



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(30) Priority Data:</b> <table style="width: 100%; border: none;"> <tr> <td style="width: 30%;">08/896,164</td> <td style="width: 30%;">17 July 1997 (17.07.97)</td> <td style="width: 40%;">US</td> </tr> <tr> <td>60/061,599</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>60/061,765</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>08/948,705</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>9721697.2</td> <td>11 October 1997 (11.10.97)</td> <td>GB</td> </tr> <tr> <td>09/102,322</td> <td>22 June 1998 (22.06.98)</td> <td>US</td> </tr> </table>			08/896,164	17 July 1997 (17.07.97)	US	60/061,599	10 October 1997 (10.10.97)	US	60/061,765	10 October 1997 (10.10.97)	US	08/948,705	10 October 1997 (10.10.97)	US	9721697.2	11 October 1997 (11.10.97)	GB	09/102,322	22 June 1998 (22.06.98)	US															
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<b>(57) Abstract</b> Various molecules associated with cancer are disclosed. The invention also discloses diagnostic and therapeutic methods based upon these molecules.																																			

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## **CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES**

### **Field of the Invention**

The invention relates to nucleic acids and encoded polypeptides which are cancer  
5 associated antigens expressed in patients afflicted with breast cancer. The invention also relates  
to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules,  
polypeptides coded for by such molecules and peptides derived therefrom, as well as related  
antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and therapeutic  
contexts.

### **Background of the Invention**

The mechanism by which T cells recognize foreign materials has been implicated in  
cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous  
melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been  
15 described. In many instances, the antigens recognized by these clones have been  
characterized.

The use of autologous CTLs for identifying tumor antigens requires that the target cells  
which express the antigens can be cultured *in vitro* and that stable lines of autologous CTL  
clones which recognize the antigen-expressing cells can be isolated and propagated. While this  
20 approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers  
including breast and colon cancer, have proved refractory to the approach.

More recently another approach to the problem has been described by Sahin et al. (*Proc.  
Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous antisera  
are used to identify immunogenic protein antigens expressed in cancer cells by screening  
25 expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified  
have been found to have elicited an high-titer humoral immune response in the patients from  
which the antisera were obtained. Such a high-titer IgG response implies helper T cell  
recognition of the detected antigen. These tumor antigens can then be screened for the presence  
of MHC/HLA class I and class II motifs and reactivity with CTLs

30 The invention is elaborated upon in the disclosure which follows.

### Summary of the Invention

Autologous antibody screening has now been applied to cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those  
5 molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis, monitoring, research, or treatment of  
10 conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of many genes, some previously known and many previously unknown, which are expressed in individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments  
15 thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be  
20 used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can involve 2, 3, 4, 5... to as many as 25, 50, 100 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a  
25 plurality of such materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such  
30 combinations: those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses.

including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer.

- 5 Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

- 15 In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 17 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 17 nucleic acids, (g) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (I) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 17 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide.

According to another embodiment the nucleic acid molecule is one of the following: a NA Group 3 molecule, a NA Group 11 molecule, a NA Group 12 molecule, a NA Group 13 molecule, a NA Group 14 molecule, a NA Group 15 molecule, or a NA Group 16 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

5 In another embodiment the agent is selected from the group consisting of (1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional  
10 variant thereof, and an HLA molecule.

The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer  
15 associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide. The cell can express one or both of the polypeptide and HLA molecule recombinantly. In another preferred embodiment the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a different human cancer associated antigen or  
20 functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also includes an adjuvant.

25 According to another aspect the invention, a composition is provided of an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 3 polypeptide, a PP Group 11 polypeptide, a PP Group 12 polypeptide, a PP Group 13 polypeptide, a PP Group 14 polypeptide, a PP Group 15 polypeptide, and a PP Group 16 polypeptide. In other  
30 embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

5       The invention in another aspect is a pharmaceutical composition of an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid  
10   molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated  
15   nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

20       In another embodiment the isolated polypeptide comprises at least two different polypeptides, each comprising a different cancer associated antigen. In separate embodiments the isolated polypeptides are selected from the following: PP Group 11 polypeptides or HLA binding fragments thereof, PP Group 12 polypeptides or HLA binding fragments thereof, PP Group 13 polypeptides or HLA binding fragments thereof, PP Group 14 polypeptides or HLA  
25   binding fragments thereof, PP Group 15 polypeptides or HLA binding fragments thereof, or PP Group 16 polypeptides or HLA binding fragments thereof.

In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA  
30   Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule. In separate embodiments the isolated nucleic acid molecules are selected from the following: a Group 11 molecule or a functional fragment

thereof, a Group 12 molecule or a functional fragment thereof, a Group 13 molecule or a functional fragment thereof, a Group 14 molecule or a functional fragment thereof, a Group 15 molecule or a functional fragment thereof, or a Group 16 molecule or a functional fragment thereof.

5           The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID numbered below and comprising all nucleic acid sequences among SEQ ID NOs 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a sequence of  
10           contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of the sequence Group 1, (2) complements of (1), and (3) fragments of (1) and (2).

          In one embodiment the sequence of contiguous nucleotides is selected from the group  
15           consisting of: (1) at least two contiguous nucleotides nonidentical to the sequence Group 1, (2) at least three contiguous nucleotides nonidentical to the sequence Group 1, (3) at least four contiguous nucleotides nonidentical to the sequence Group 1, (4) at least five contiguous  
          nucleotides nonidentical to the sequence Group 1, (5) at least six contiguous nucleotides nonidentical to the sequence Group 1, or (6) at least seven contiguous nucleotides nonidentical  
20           to the sequence Group 1.

          In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18  
          nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30  
          nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides  
25           and every integer length therebetween.

          In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

          Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

30           According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule

and a nucleic acid encoding an MHC, preferably HLA, molecule.

In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

5 In another aspect the invention is a host cell transformed or transfected with an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and further comprising a nucleic acid encoding HLA.

10 According to another aspect of the invention an isolated polypeptide encoded by the isolated nucleic acid molecules the invention, described above, is provided. These include PP Group 1-17 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA or a human antibody.

15 The invention includes in another aspect an isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length  
20 to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from  
25 the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of ("a"), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

30 According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent.



which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (i) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously

expresses an HLA molecule which binds the human cancer associated antigen.

The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) identifying a nucleic acid molecule expressed by  
5 the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a cancer associated antigen. (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected  
10 host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC  
15 molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to  
20 render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated  
25 antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the  
30 step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein.

The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (i) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein. In another embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The invention includes in another aspect a composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid

sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter  
5 includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (I) a peptide derived from a protein encoded by a nucleic acid molecule that is a  
10 NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular medicament is for  
15 treating cancer and a more particular medicament is for treating breast cancer, lung cancer, renal cancer, colon cancer, prostate cancer or gastric cancer.

### **Detailed Description of the Invention**

In the above summary and in the ensuing description, lists of sequences are provided.  
20 The lists are meant to embrace each single sequence separately, two or more sequences together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the  
25 sequence (-1 so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the  
30 coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing, and the predicted amino acid sequences of some clones also are presented. Of the foregoing, it can be seen that some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched. Other clones are novel but have some homology to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not known that the gene was associated with cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

#### "Nucleic Acid Sequences"

NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs 1-816 and which code for a cancer associated antigen precursor.

(b) deletions, additions and substitutions which code for a respective cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

5 (d) complements of (a), (b) or (c).

NA Group 2. Fragments of NA Group 1, which codes for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by a an autologous antibody or lymphocyte.

10

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor.

15

(b) deletions, additions and substitutions which code for a respective human cancer associated antigen precursor.

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

20

NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

25

NA Group 6. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

30

NA Group 7. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

- 15 -

NA Group 8. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 9. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human  
5 renal cancer associated antigen precursor.

NA Group 10. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

10 NA Group 11. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 12. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

15

NA Group 13. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 14. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human  
20 lung cancer associated antigen precursor.

NA Group 15. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

25 NA Group 16. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 17. A subset of NA Group 1, comprising human cancer associated antigens that react with allogenic cancer antisera.

30

#### Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

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- PP Group 2. Polypeptides encoded by NA Group 2
- PP Group 3. Polypeptides encoded by NA Group 3.
- PP Group 4. Polypeptides encoded by NA Group 4.
- PP Group 5. Polypeptides encoded by NA Group 5.
- 5 PP Group 6. Polypeptides encoded by NA Group 6.
- PP Group 7. Polypeptides encoded by NA Group 7.
- PP Group 8. Polypeptides encoded by NA Group 8.
- PP Group 9. Polypeptides encoded by NA Group 9.
- PP Group 10. Polypeptides encoded by NA Group 10.
- 10 PP Group 11. Polypeptides encoded by NA Group 11.
- PP Group 12. Polypeptides encoded by NA Group 12.
- PP Group 13. Polypeptides encoded by NA Group 13.
- PP Group 14. Polypeptides encoded by NA Group 14.
- PP Group 15. Polypeptides encoded by NA Group 15.
- 15 PP Group 16. Polypeptides encoded by NA Group 16.
- PP Group 17. Polypeptides encoded by NA Group 17.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second  
20 Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02%  
25 Bovine Serum Albumin, 2.5mM NaH<sub>2</sub>PO<sub>4</sub>(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

30 There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to



manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by  
5 isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60%  
10 nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the internet (<ftp://ncbi.nlm.nih.gov/pub/>). Exemplary tools include the BLAST system available at <http://www.ncbi.nlm.nih.gov>. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained  
15 using the MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect  
20 the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions (see also the Examples) can be performed on samples taken from breast cancer patients or subjects suspected of having a condition characterized by expression of breast cancer associated antigen genes. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences  
25 presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast cancer associated genes correspond to SEQ ID NOs. 1-40 and 66. The preferred breast cancer associated antigens for the methods of diagnosis disclosed herein are those set forth in SEQ ID NOs:[31, 33 and 34], which were found to react with allogeneic breast  
30 cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The colon cancer associated genes correspond to SEQ ID Nos. 544-586, even numbers

only. The preferred colon cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic colon cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The gastric cancer associated genes correspond to SEQ ID NOs 176-436 and 588-674.

- 5 The preferred gastric cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic gastric cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The renal cancer associated genes correspond to SEQ ID Nos. 89-169, odd numbers only, and 170, 172, and 174. The preferred renal cancer associated antigens for the methods of  
10 diagnosis disclosed herein are those, which were found to react with allogeneic renal cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The lung cancer associated genes correspond to SEQ ID Nos. 689, 691, 692, 694, 696-707, 709, 711, and 712. The preferred lung cancer associated antigens for the methods of  
15 diagnosis disclosed herein are those, which were found to react with allogeneic lung cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The prostate cancer associated genes correspond to SEQ ID NOs 437-543. The preferred prostate cancer associated antigens for the methods of diagnosis disclosed herein are those,  
20 which were found to react with allogeneic prostate cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of  
25 encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating breast cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA, CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine  
30 codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus,

the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger  
5 nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of GenBank  
10 accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing  
15 GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

20 Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins for generating  
25 antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic  
30 purposes as described in greater detail below.

As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long, up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last nucleotide, (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 18 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed. Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g.,* Thomson et al., *Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generated individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7,

MAGE-8, MAGE-9, MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen phosphorylase, Melan-A, and MAGE-C1. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990).for example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient (for examples of this, see the Examples below).

Polytopes can be prepared which correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J.*

*Immunol.* 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

5 In instances in which a human HLA class I molecule presents tumor rejection antigens derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the  
10 vector contains both coding sequences, the single vector can be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected. The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a  
15 cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

20 As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide, to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of  
25 one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby,  
30 inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules

are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the sequences of nucleic acids encoding breast cancer associated antigen, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding breast cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end

of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

5 In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which  
10 (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters,  
15 alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamides, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other  
20 than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding  
25 breast cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense  
30 oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term



“pharmaceutically acceptable” means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term “physiologically acceptable” refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

As used herein, a “vector” may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g.,  $\beta$ -galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be “operably” joined

when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a breast cancer associated antigen polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the

human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1 $\alpha$ , which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996). Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed breast cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a breast cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a breast cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the breast cancer associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the breast cancer associated antigen nucleic acid, in an arrangement which permits amplification of the breast cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and partial

proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed  
5 recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

10 A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of breast cancer associated antigens will require longer segments to be unique while others  
15 will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more, including each integer up to the full length, amino acids long).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or  
20 fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family  
25 members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated  
30 antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to

a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a breast cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of

a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred  
5 codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer  
10 associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant  
15 polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino  
20 acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor,  
25 New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of SEQ ID proteins disclosed herein. Conservative substitutions of amino acids include  
30 substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

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For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs (e.g., as described in the Examples), one can make conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amato and Drijfhout (D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC. These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

The invention as described herein has a number of uses, some of which are described elsewhere herein. First, the invention permits isolation of the cancer associated antigen protein

molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant



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negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolate cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York; Roitt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications, Oxford). The

pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an F(ab')<sub>2</sub> fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for F(ab')<sub>2</sub>, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous

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human or non-human sequences; chimeric F(ab')<sub>2</sub> fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer

associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technitium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminogluthethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon- $\alpha$ , lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer associated antigens are expressed. An example of such a disorder is cancer, breast, colon, gastric,

renal, prostate and lung cancers as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

5 In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include CD34<sup>+</sup> hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the  
10 immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by a  
15 subject's immune system, leading to lysis of antigen presenting cells, such as breast cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a method for T cell differentiation is presented in International  
20 Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell of the type described herein. These transfectants present the desired complex of their surface and, when combined with a CTL of interest, stimulate its proliferation. COS cells, such as those used herein are widely available, as are  
25 other suitable host cells. Specific production of a CTL clone is described herein, and is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL  
30 clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of  $\beta_2$ -

microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio of 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddel et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-1410, 1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the invention. CTLs can also be provoked *in vivo*, using a number of approaches. One approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114, 1991) exemplifies this approach, showing the use of transfected cells expressing HPV E7 peptides in a therapeutic

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regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a breast cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigen, as described elsewhere herein. Nucleic acids encoding a cancer associated antigen also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a Vaccinia virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The breast cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, such as the nucleic acids (and encoded polypeptides and peptides) of SEQ ID NO:31,33 and 34 and others, for example, shown in the examples below.

The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating an immune response against an antigen. It does not require elimination or eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against breast cancer using a cancer associated antigen nucleic acid. For example, cancer cells can be introduced into a mouse to create a tumor, and one or more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor

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size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization include the administration of one or more cancer associated antigen polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 µg to about 100 µg. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.



Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (*see, e.g., Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation, Zheng P., et al. *PNAS* 95 (11) 6284-6289 (1998).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity, Gajewski et al., *J. Immunol*, 154:5637-5648 (1995). Tumor cell transfection with B7 has been discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., *J Immunol*, 154:1-8 (1986). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization Kim J., et al. *Nat Biotechnol.*, 15:7:641-646 (1997) and recombinant viruses such as adeno and pox (Wendtner et al., *Gene Ther*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations. The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be

considered.

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother*, 21:2:95-108 (1989).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Fenton et al., *J. Immunother*, 21:2:95-108 (1998). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCS, Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to enhance a response to tumor antigens which are normally encountered outside of a inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes have not been defined within known TRA precursors.

A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner which can interact with cancer associated antigen polypeptides is present in the solution,

then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these  
5 prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The  
10 expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of  
15 nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a breast cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and  
20 returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and  
25 targeted liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of  
30 viruses and virus-like particles which have been used to deliver exogenous nucleic acids include:

replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol* 71:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venezuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for

producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene  
5 Transfer and Expression, A Laboratory Manual," W.H. Freeman C.O., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the  
10 surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid-CaPO<sub>4</sub> precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic  
15 acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or  
20 incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer associated antigen, alone or as a complex with a MHC molecule.

Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation for targeting and/or to facilitate  
25 uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

30 When administered, the therapeutic compositions of the present invention can be

administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

5        The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of  
10 skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue  
15 experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer  
20 associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as cancer, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to  
25 diagnostic methods of the invention discussed herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and  
30 weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of

administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of breast cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system as described herein, by measuring downstream effects such as gene expression, or by measuring the physiological effects of the breast cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100  $\mu$ g, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen of variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer

associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

As part of the immunization compositions, the peptide antigens are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Where cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein. Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier.

When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable compositions. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the



effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

A breast cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

Compositions suitable for oral administration may be presented as discrete units, such as

capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of breast cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

### Examples

#### **Example 1: Preparation of breast cancer cDNA expression libraries**

Step 1: Purification of total RNA from tumors.

Total RNA was isolated from tumor samples using the guanidium thiocyanate-phenol-chloroform extraction protocol described by Chomczynski and Sacci (*Anal. Biochem.* 162:156-159, 1987).

Step 2: Purification of mRNA.

A Dynabeads mRNA isolation kit (Dyna, Cat.No. 610.01) was used to isolate mRNA from the pool of total RNA isolated in step 1 above according to the manufacturer's instructions.

Step 3: cDNA synthesis.

cDNA synthesis was performed using a ZAP-cDNA synthesis Kit (Stratagene, La Jolla CA; Cat. No. 200400) according to the manufacturer's protocol. A specific linker-primer which contains a XbaI cloning site was designed and used in this protocol, to facilitate subcloning into TriplEx

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vector. The sequence of the primer was:

GAGAGAGAGAGAGAGAGAGAAGTCGACTCTAGATTTTTTTTTTTTTTTTTT-Xba I site

Step 4: Ligation into the TriplEx vector arms.

5 The cDNAs generated in step 3 above were ligated into TriplEx vector arms (Clontech, Palo Alto, CA; Cat. No. 6162-1); the arms were predigested with EcoR I/Xba I.

Step 5: Packaging into phages with Gigapack III kit.

The ligation mix (TriplEx/cDNA) from step 4 was packed into phages using the Gigapack III Gold Cloning Kit (Stratagene, Cat. N.200450) according to the protocol supplied with the kit.

10 Step 6: Titering and amplification of generated libraries was performed according to the Stratagene protocols.

The foregoing protocol was used to prepare several libraries from tumor sample of different patients. Some libraries were prepared using the UNI-ZAP XR vector system (Stratagene)  
15 according to the manufacturer's protocol, and some using the TriplEx system as described above.

Table 2

UNI-ZAP Libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
20 HBR173	$1.8 \times 10^6$ pfu	Ductal Carcinoma, Grade III
HBR184	$3.5 \times 10^6$ pfu	Invasive Ductal Carcinoma, Grade II
TriplEx libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	$2.3 \times 10^6$ pfu	Ductal Carcinoma, Grade III
25 HBR184	$1.1 \times 10^6$ pfu	Invasive Ductal Carcinoma, Grade II
HBR257	$2.5 \times 10^6$ pfu	Invasive Ductal Carcinoma, Grade II
HBR297	$4.0 \times 10^6$ pfu	Ductal Carcinoma, Grade II
HBR248	$1.0 \times 10^6$ pfu	Invasive Ductal Carcinoma with Vascular Permeation, Grade III

HBR271	$2.5 \times 10^6$ pfu	Medullary Carcinoma
HBR263	$10.0 \times 10^6$ pfu	Inv. Pleiomorphic Lobular Carcinoma, Grade II

All libraries were screened with the exception of HBR173 (no autologous serum). No  
5 serum-positive clones were found by screening HBR271 library.

### Example 2: Immunoscreening

Sera was obtained from donors undergoing routine diagnostic and therapeutic procedures. It was stored at  $-70^{\circ}\text{C}$  prior to absorption. Sera, at a dilution of 1:10 in Tris buffered saline (TBS, pH  
10 7.5), was sequentially passed through Sepharose 4B columns which had been coupled to lysates from *E. coli* Y1090 and bacteriophage infected *E. coli* BNN97 (5 Prime 3 Prime, Inc. Boulder, Co.). Final serum dilutions were prepared in 0.2% non-fat dried milk/TBS (NFDM) and stored at  $4^{\circ}\text{C}$ . Library screening was performed as described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995) with following modifications. Recombinant phage at a concentration of 4 x  
15  $10^3$  per 15 cm plate were amplified for 6 hours and transferred to nitrocellulose membranes for an additional 15 hours at  $37^{\circ}\text{C}$ . Membranes were then blocked with 5% NFDM. As an alternative to generation of IgG subtracted libraries, membranes were pre-screened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific, goat anti-human IgG (Jackson ImmunoResearch Laboratories Inc., West Grove, PA) for 1 hour at room temperature. Color was developed with 3,3'  
20 diaminobenzidine tetrahydrochloride and IgG encoding clones were scored. Membranes were then incubated in a 1:100 dilution of absorbed autologous sera for 15 hours at room temperature. Following serum exposure, filters were incubated in a 1:3000 dilution of alkaline phosphatase conjugated, Fc fragment specific, goat anti-human IgG (Jackson ImmunoResearch Laboratories Inc.) for 1 hour at room temperature and processed for 4-nitro blue tetrazolium  
25 chloride/5-bromo-4-chloro-3-indolyl-phosphate color development. Serum positive clones were subcloned and retested for serum reactivity as above except nitrocellulose transfer was decreased to 3 hours. For the determination of allogeneic serum reactivity, plates containing an equal number of serum positive clones and negative control plaques were similarly processed less the IgG prescreening steps. A minimum of  $5 \times 10^5$  recombinants were screened per cDNA library, a number

which approximates a point at which the likelihood of repeat isolations of previously identified clones outweigh the prospect of identifying new clones.

### Example 3: DNA Sequencing

- 5            Phage cDNA clones were converted to pBKCMV phagemid forms by in vivo excision. Plasmid DNA was purified on Qiaprep spin columns (Qiagen Inc. Chatsworth, CA) and subjected to EcoRI/XbaI restriction enzyme digestion. Clones representing different cDNA inserts were sequenced at Cornell University DNA services (Ithaca, NY) using an ABI Prism (Perkin Elmer) automated DNA sequencer. The sequences of the clones were compared with sequences in
- 10    GenBank and HGI databases to detect homologous nucleic acid and/or protein sequences. The following table lists exemplary related sequences.

Table 3: Sequences Related to Breast Cancer Associated Antigen Clones

Clone	Nucleotide Homology	Clone	Nucleotide Homology	Clone	Nucleotide Homology
15 LONY-Br-1	L34543	LONY-Br-23	AA262134, U74628	LONY-Br-44	D15057
LONY-Br-2	S75417	LONY-Br-24	AA282633	LONY-Br-45	AB000815
LONY-Br-3	J05211	LONY-Br-25	M62324	LONY-Br-46	L04733
LONY-Br-4	X15187	LONY-Br-26	M99389	LONY-Br-47	X88791
LONY-Br-5	X62083	LONY-Br-27	X79389	LONY-Br-48	AF000430
20 LONY-Br-6	J04965	LONY-Br-28	D44466	LONY-Br-49	none
LONY-Br-7	D63784	LONY-Br-29	M33197	LONY-Br-50	AA226732
LONY-Br-8	U11292	LONY-Br-30	M17886	LONY-Br-51	AA046574
LONY-Br-9	HSB06D102	LONY-Br-31	L38941	LONY-Br-52	none
LONY-Br-10	none	LONY-Br-32	X17644	LONY-Br-53	AB002307
25 LONY-Br-11	none	LONY-Br-33	X75342	92	AA127328
LONY-Br-12	AA430998	LONY-Br-33	X75342	101	AA167314
LONY-Br-13	D83032	LONY-Br-34	U43368	102	AA508139
LONY-Br-14	AA034417	LONY-Br-35	X15882	107	none
LONY-Br-15	AA167070	LONY-Br-37	AA121558	109	AA220229

LONY-Br-16	none	LONY-Br-38	AA211771	110	W67775
LONY-Br-17	AA161103	LONY-Br-39	AA367417	111	AA280070
LONY-Br-19	R13835	LONY-Br-40	AA188052	112	AF004292
LONY-Br-20	HUMORF003	LONY-Br-41	THC83518	131	none
LONY-Br-21	S74572	LONY-Br-42	none	143	AA481578
LONY-Br-22	AA070233	LONY-Br-43	HU35246	162	AA481578

#### Example 4: Reverse transcriptase (RT) PCR and Rapid Amplification of cDNA Ends (RACE)

The mRNA expression pattern of selected cDNA clones was determined by RT-PCR using a panel of normal tissue RNA. This test panel consisted of lung, testis, small intestine, colon, breast, liver, and placenta, and was purchased from Clontech Laboratories Inc. (Palo Alto, CA). Colon tumor RNA was also included in this panel and was prepared as described above. As a control for genomic DNA contamination, all cDNA synthesis reactions were set up in duplicate with the additional sample lacking reverse transcriptase. Gene specific PCR primers were designed to amplify 5' fragments of 300-400 bp and were purchased commercially (Gibco BRL, Grand Island, NY). PCR reactions were undertaken at an annealing temperature of 68°C using a Perkin Elmer thermal cycler. In certain cases, RT-PCR products were subcloned into the pCR2.1 plasmid vector (Invitrogen) and multiple clones were subjected to DNA sequencing as described. 5' and 3' RACE reactions were undertaken using gene specific and adapter primers in conjunction with Marathon Ready normal colon cDNA and KlenTaq polymerase (Clontech) as per manufacturers protocol. Products were then subcloned into the pCR2.1 plasmid vector (Invitrogen) and screened by PCR with internal primers for presence of the desired insert. Multiple RACE clones were subjected to DNA sequencing as described.

#### Example 5: Northern blot analysis

Northern blots containing the transfer yields of 2 µg poly A<sup>+</sup> RNA from a panel of normal tissues were obtained commercially (Clontech). Random primed <sup>32</sup>P labeled probes consisting of 300-600 bp PCR products from 5 prime coding sequences of serum positive cDNA clones were hybridized for 1.5 hours in Expresshyb (Clontech) at 68°C and washed at high stringency (2 times,

30 min. each, 0.1X SSC/0.1% SDS at 68°C). Resultant blots were used to expose Biomax MS autoradiography film (Eastman Kodak Co., Rochester, NY).

Table 4: Breast Cancer Associated Antigen Clone mRNA sizes

Clone	Size (kb)	Clone	Size (kb)	Clone	Size (kb)
LONY-Br-1	1.8	LONY-Br-17	1.0	LONY-Br-33	2.6
LONY-Br-2	2.9	LONY-Br-19	1.5	LONY-Br-34	2.1
LONY-Br-3	4.8	LONY-Br-20	2.4	LONY-Br-35	1.9
LONY-Br-4	1.2	LONY-Br-21	2.4	LONY-Br-36	0.8
LONY-Br-5	0.9	LONY-Br-22	1.6	LONY-Br-37	1.0
LONY-Br-6	1.4	LONY-Br-23	1.3	LONY-Br-38	2.2
LONY-Br-7	1.3	LONY-Br-24	3.9	LONY-Br-39	1.9
LONY-Br-8	0.9	LONY-Br-25	1.9	LONY-Br-40	3.4
LONY-Br-9	6.0	LONY-Br-26	1.5	LONY-Br-41	3.9
LONY-Br-10	3.6	LONY-Br-27	1.2	LONY-Br-42	0.6
LONY-Br-11	4.6	LONY-Br-28	0.5	LONY-Br-43	1.4
LONY-Br-12	2.2	LONY-Br-29	0.6	LONY-Br-44	0.7
LONY-Br-13	1.2	LONY-Br-30	0.8	LONY-Br-45	3.0
LONY-Br-14	0.8	LONY-Br-31	0.4	LONY-Br-46	3.7
LONY-Br-15	0.9	LONY-Br-32	2.2	LONY-Br-47	0.5
LONY-Br-16	2.5	LONY-Br-33	2.6	LONY-Br-48	1.6

#### **Example 6: Isolation of gastric and prostate clones**

A stomach cancer cDNA library was established, using standard techniques, then the library was screened, using the SEREX methodology described supra, and set forth by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), incorporated by reference in their entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M guanidium thiocyanate/0.5% sodium N-lauryl sarcosine/ and 25 mM EDTA followed by centrifugation in 5.7 M CsCl/25 mM sodium acetate/10 uM EDTA at 320,000 rpm. Total mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed

by taking 5 ug of mRNA, using standard methodologies to reverse transcribe the material.

Libraries were prepared from four different stomach cancer patients, referred to as "SM", "CK" and "SS" and "KM" respectively. A total of  $2.5 \times 10^6$ ,  $1.1 \times 10^6$ , and  $1.7 \times 10^6$  cDNA clones were obtained from the "SM", "CK" and "SS" individuals. Additional libraries were prepared from prostate cancer patient "OT".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF E. coli, and incubated for eight hours at 37°C. A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane was then washed, four times, without TBS which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of human antibody (1:2000, diluted in TBS with 1% BSA. The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times with TBS. Those clones which produced antibodies were visualized with 0.06%, 3,3'-diamino benzidine tetrachloride, and 0.015%  $H_2O_2$ , in 50 mM Tris (pH 7.5). Any clones which produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C. The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02%  $Na_3N$ . The serum had been treated to remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of E. coli Y1090 had been attached, followed by passage over a second column which had E. coli lysate and lysate of E. coli infected with lambda bacteriophage. The screening was carried out five times. The samples were then diluted to 50 ml, and kept at -80°C, until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the POD labelled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, a total of 36 clones were resolved into known and unknown genes. In the table that follows, the "+" and "-" signs are essentially used to compare signals to each other. All were positive. Table 5, which follows, summarizes some of this



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work isolation and sequencing of "SM" clones. Specifically, with reference to the first page of the table, previously identified human proteins and the nucleotide sequences, set forth in SEQ ID NOS:588-626 are known. The four molecules which follow in SEQ ID NOS:627-634 (gelsolin, zinc finger protein family, variant zinc finger motif protein goliath and homeodomain proteins), have not been identified in humans previously, although there are related molecules found in other species. Finally, with reference to Table 5, the last four moieties, i.e., prepro- $\alpha$  collagen, heterogeneous ribonucleoprotein D, nucleosome assembly protein 2, and NY-ESO-2/Ulsn NRP/V1 small nuclear ribonucleoprotein, are also known. Nucleotide sequences are set forth at SEQ ID NOS:635-642. The nucleic acid molecules having the nucleotide sequences set forth at SEQ ID NOS:643-670 represent molecules for which no related sequences were found. SEQ ID NO:671 combines the sequences of SEQ ID NOS:627-630, inclusive. SEQ ID NO:672 combines SEQ ID NOS:643-656, SEQ ID NO:673 combines SEQ ID NOS:657, 659 and 662, while SEQ ID NO:674 combines SEQ ID NOS: 658, 660, 661 and 663.

SEREX analysis of clones from libraries derived from patients "CK", "SS", "KM" (all gastric cancer) and patient "OT" (prostate cancer) was carried out as described above. The nucleotide sequences of clones derived from gastric cancer patients are presented as SEQ ID NOS:176-436. The nucleotide sequences of clones derived from prostate cancer patient "OT" are presented as SEQ ID Nos:437-543.

#### **Example 7: Isolation and analysis of colon clones**

Colon tumor samples were obtained as surgical samples, and were frozen at -80°C until ready for use.

Total RNA was then isolated from the samples, using the guanidium thiocyanate method of Chirgwin, et al., *Biochemistry* 18: 5294-5299 (1979), incorporated by reference. The total RNA thus obtained was then purified to isolate all poly A<sup>+</sup> RNA, using commercially available products designed for this purpose.

The poly A<sup>+</sup> RNA was then converted into cDNA, and ligated into  $\lambda$ ZAP, a commercially available expression vector, according to the manufacturer's suggested protocol.

Three cDNA libraries were constructed in this way, using colorectal carcinoma samples.

A fourth library, also from colorectal carcinoma, was prepared, albeit in a different way. The

fourth library was an IgG subtraction library, prepared by using a subtraction partner, generated by PCR amplification of a cDNA clone which encoded an IgG molecule. *See, e.g., Ace et al, Endocrinology* 134: 1305-1309 (1994), and incorporated by reference in its entirety. IgG subtraction is done to eliminate any false, positive signals resulting from interaction of cDNA clones which encode IgG, with the IgG then interacting with the anti-human IgG used in the SEREX assay, as described herein. PCR products were biotinylated, and hybridized with denatured second strand cDNA, at 68°C for 18 hours. Biotinylated hybrid molecules were coupled to streptavidin, and then removed by phenol chloroform extraction. Any remaining cDNA was also ligated into  $\lambda$ ZAP. All libraries were amplified, prior to immunoscreening.

Immunoscreening was carried out using sera obtained from patients undergoing routine diagnostic and therapeutic procedures. The sera were stored at -70°C prior to use. Upon thawing, the sera were diluted at 1:10 in Tris buffered saline (pH 7.5), and were then passed through Sepharose 4B columns. First, the sera were passed through columns which had *E. coli* Y1090 lysates coupled thereto, and then lysates from bacteriophage infected *E. coli* BNN97 lysates. Final serum dilutions were then prepared in 0.2% non-fat dried milk/Tris buffered saline.

The method of Sahin et al., *Proc. Natl. Acad. Sci. USA* 92:11810-11813 (1995), and U.S. Patent No. 5,698,396, both of which are incorporated by reference, was used, with some modifications. Specifically, recombinant phages at a concentration of  $4 \times 10^3$  phages per 15 cm plate (pfus), were amplified for six hours, after which they were transferred to nitrocellulose membranes for 15 hours. The membranes then were blocked with 5% nonfat dried milk.

As an alternative to the IgG subtraction procedure discussed above, membranes were prescreened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific goat anti-human IgG, for one hour, at room temperature. Color was developed using 3,3'-diaminobenzidine tetrahydrochloride, which permitted scoring of IgG encoding clones.

Membranes were then incubated in 1:100 dilutions of autologous sera, which had been pretreated with the Sepharose 4B columns, as described *supra*. The filters were then incubated, in a 1:3000 dilution of alkaline phosphatase conjugated Fc fragment specific, goat anti-human IgG, for one hour, at room temperature. The indicator system 4-nitroblue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate was then added, and color development assessed. Any positive clones were subcloned, and retested, except the time on the nitrocellulose membrane was reduced to three

hours.

Positive clones were isolated and sequenced according to standard procedures. The nucleotide sequences of the clones are set forth in the even numbered sequences from SEQ ID Nos:544-586. The odd numbered sequences from SEQ ID Nos:545-587 represent the translated amino acid sequences of the colon nucleic acid clones. Analysis of probes for SEQ ID NOS:544 and 546 confirmed their universal expression.

The foregoing results reflect SEREX isolation of colon cancer clones using autologous serum. The positive clones were then rescreened, using allogeneic serum, following the same method discussed supra, in example 2, except IgG prescreening was omitted. The allogeneic sera was obtained from sixteen normal blood donors, and twenty nine patients who had been diagnosed with colorectal cancer.

The analysis with the two types of serum revealed that fourteen reacted with a subset of sera from normal and cancer patients, twenty-eight only with autologous sera, and six with both allogeneic and autologous sera. Over 60% of the allogeneic serum samples tested reacted with at least one of these positive clones. About 20% reacted with two or more.

In view of the results described above, further experiments were carried out using serum samples from patients with other forms of cancer, i.e., renal cancer (13 samples), lung cancer (23 samples), and breast cancer (10 samples). The results are set forth in Table 6 which follows:

Table 6: Allogeneic serotyping using colon cancer clones

Clone Number	Normal Sera	Colon Cancer	Renal Cancer	Lung Cancer	Breast Cancer
NY-Co-8	0/16	8/29	1/13	0/23	0/10
NY-Co-9	0/16	5/29	1/13	1/23	0/10
NY-Co-13	0/16	5/29	0/13	0/23	0/10
NY-Co-16	0/16	3/29	0/13	0/23	0/10
NY-Co-20	0/16	4/29	0/13	0/23	0/10
NY-Co-38	0/16	4/29	3/13	0/23	1/10

Of the six clones which were identified as being reactive with autologous and allogeneic

cancer serum, and not with normal serum, two were found to be identical to previously identified molecules (NY-Co-. Four others were found to have little or no homology to known sequences and thus are preferred allogeneic-reactive colon cancer clones. These nucleic acids and their polypeptide translations are presented as SEQ ID NOS: 544-551: SEQ ID NO: 544/545 (NY-CO-8), SEQ ID NO: 546/547 (NY-CO-9), SEQ ID NO: 548/549 (NY-CO-16) and SEQ ID NO: 550/551 (NY-CO-38). . Of twenty seven allogeneic colon cancer serum samples tested, 67% reacted with at least one of these antigens.

The expression pattern of mRNA corresponding to SEQ ID NOS:544, 546 and 550, as well as other sequences identified via the preceding examples was determined. To do this, RT-PCR was carried out on a panel of RNA samples, taken from normal tissue. The panel contained RNA of lung, testis, small intestine, colon, breast, liver and placenta tissues. The RNA was purchased from a commercial source. RNA from a colon tumor sample was also included. All samples were set up for duplicate runs, so that genomic DNA contamination could be accounted for. In the controls, no reverse transcriptase was used.

Primers were designed which were specific for the cDNA, which would amplify 5'-fragments, from 300-400 base pairs in length. The PCR reactions were undertaken at an annealing temperature of 68°C. Where appropriate, 5' and 3'-RACE reactions were undertaken, using gene specific primers, and adapter primers, together with commercially available reagents. Specifically, SEQ ID NOS: 546 and 550 were tested using RACE. The resulting products were subcloned into vector pCR 2.1, screened via PCR using internal primers, and then sequenced.

SEQ ID NOS:544 and 546 were found to be amplified in all tissues tested. SEQ ID NO:550 was found in colon tumor, colon metastasis, gastric cancer, renal cancer and colon cancer cell lines Colo 204 and HT29, as well as in normal colon, small intestine, brain, stomach, testis, pancreas, liver, lung, heart, fetal brain, mammary gland, bladder, adrenal gland tissues. It is was not found in normal uterine, skeletal muscle, peripheral blood lymphocytes, placental, spleen thymus, or esophagus tissue, nor in lung cancer.

The analysis also identified differential expression of a splice variant of SEQ ID NO:550, i.e., SEQ ID NO:552. When the two sequences were compared, it was found that SEQ ID NO:550 encodes a putative protein of 652 amino acids (SEQ ID NO:551), and molecular weight of 73,337 daltons. SEQ ID NO:552, in contrast, lacks an internal 74 base pairs, corresponding to

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nucleotides 1307-1380 of SEQ ID NO:550. The deletion results in formation of a stop codon at the splice function, and a putative protein of 403 amino acids (SEQ ID NO:553), and molecular weight 45,839. The missing segment results in the putative protein lacking a PEST protein degradation sequence, thereby suggesting a longer half life for this protein.

5 In additional experiments, primers designed not to differentiate between SEQ ID NOS: 550 and 552 resulted in almost universal amplification (placenta being the only exception). In contrast, when primers specific for SEQ ID NO:552 were used differences were seen in normal pancreatic, liver, lung, heart, fetal brain, mammary gland, bladder, and adrenal gland tissue, where there was no expression of SEQ ID NO:552 found.

10 Northern blotting was also carried out for SEQ ID NOS: 544, 546, 550 and 552. These experiments employed the same commercially available RNA libraries discussed above were used.

Samples (2 ug) of polyA<sup>+</sup> RNA were analyzed from these samples, using random, <sup>32</sup>P labelled probes 300-360 nucleotides in length, obtained from PCR products. These probes were hybridized to the RNA, for 1.5 hours, at 68°C, followed by two washes at 0.1xSSC, 0.1% SDS, 15 68°C, for 30 minutes each time.

SEQ ID NOS:544 and 546 were again found to be universally expressed.

Further screening identified additional isoforms of SEQ ID NOS:544 and 550. These are set forth as SEQ ID NOS: 554, 556, 558 and 560. The isoform represented by SEQ ID NO:554, (translated as SEQ ID NO:555) is a naturally occurring splice variant of SEQ ID NO:544, found 20 in normal colon. SEQ ID NO:556 (translated as SEQ ID NO:557), which is an isoform of SEQ ID NO:550 (translated as SEQ ID NO:551), was found in brain tissue, primarily spinal chord and medulla. SEQ ID NO:558 (translated as SEQ ID NO:559), was found in normal kidney and in colon tumors, metastasized colon cancer, renal cancer, gastric cancer, and in colon cancer cell line Colo 205. It was not found in any normal tissue other than kidney.

25 The nucleic acid molecule whose nucleotide sequence set forth as SEQ ID NO:560 (translated as SEQ ID NO:561), is a further isoform of SEQ ID NO:552. It is similar to SEQ ID NO:558, except it contains a long nucleotide insert encoding a longer COOH terminus. It was expressed in normal bladder and kidney cells, and renal cancer cells. It was not expressed in colon cancer cells.

30 It is reported above that fourteen clones reacted with subsets of serum from both normal

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and cancer patients, while twenty eight reacted with autologous sera only. These clones were sequenced, in accordance with standard, art recognized methods. Of the clones which reacted only with autologous sera, nine appear to be previously unidentified sequences. These are set forth as SEQ ID NOS: 562, 564, 566, 568, 570, 572, 574, 576 and 578. SEQ ID NO:562 (translated as SEQ ID NO:563) is 1445 nucleotides long, and shows some similarity to known sequences for myosin and tropomyosin. SEQ ID NO:564 (translated as SEQ ID NO:565), which is 1226 nucleotides long, contains a TPR motif. The sequence set forth in SEQ ID NO:566 (translated as SEQ ID NO:567) is 1857 nucleotides long, and shows similarity to cyclophilins. The nucleotide sequence set forth in SEQ ID NO:568 (translated as SEQ ID NO:569) is 1537 nucleotides long, and shows similarity to murine gene 22A3, which has unknown function, but resembles an unconventional form of myosin, as well as an EST for heat shock inducible mRNA. As for the molecule set forth in SEQ ID NO:570 (translated as SEQ ID NO:571), it appears to resemble a nucleic targeting signal protein. SEQ ID NO: 572 (translated as SEQ ID NO:573) is 604 nucleotides long, and may encode a lysosomal protein. The molecule set forth in SEQ ID NO:574 (translated as SEQ ID NO:575) is 742 nucleotides long, and encodes a protein with an SH3 domain and which shows some similarity to GRB2 and human neutrophil oxidase factor. The molecule set forth in SEQ ID NO:576 (translated as SEQ ID NO:577) is 1087 nucleotides long, and encodes a protein which contains coiled core domains. The molecule set forth in SEQ ID NO:578 (translated as SEQ ID NO:579) is 2569 nucleotides long, shows some similarity with *Drosophila* homeotic material tudor protein, and has a DY(F)GN repeat.

Additional sequences were identified which were expressed in both normal sera and cancer cells. The sequence set forth in SEQ ID NO:580 (translated as SEQ ID NO:581), e.g., is 2077 nucleotides long, and was expressed by both colorectal cancer and normal cells. Analysis of the sequence showed that it possesses a nuclear targeting sequence. The molecule set forth in SEQ ID NO:582 (translated as SEQ ID NO:583) is 3309 nucleotides long, was expressed by colorectal cancer and normal cells, and is similar to heat shock protein 110 family members. The molecule presented in SEQ ID NO:584 (translated as SEQ ID NO:585) was expressed in a colon to lung metastasis, as well as by normal tissue. It is 2918 nucleotides in length. Analysis shows that it contains 2 zinc finger domains. The nucleotide sequence of SEQ ID NO:586 (translated as SEQ ID NO:587) was also expressed in a colon to lung metastasis, is 1898 nucleotides long, and is

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also expressed by normal tissue. Specifically, the reactivity of the molecules was as follows:

Table 7

5	SEQ ID NO:	Normal Sera Reactivity	Tumor Sera Reactivity
	580	2/16	2/16
	582	2/16	3/16
10	584	2/16	2/16
	586	2/8	1/16

A more extensive set of RT-PCR experiments were carried out to study the expression pattern of SEQ ID NOS: 550, 552, 558 and 560. The results follow.

15

Table 8: RT-PCR analysis of colon SEREX clones

	<u>normal tissue</u>	<u>SEQ ID NO.:550</u>	<u>SEQ ID NO.:552</u>	<u>SEQ ID NO.:558</u>	<u>SEQ ID NO.:560</u>
20	kidney	+	Negative	Negative	Negative
	colon	+	Negative	Negative	Negative
	small		Negative	Negative	Negative
	intest.	+	Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
25	stomach	+	Negative	Negative	Negative
	testis	+	Negative	Negative	Negative
	pancreas	+	Negative	Negative	Negative
	lung	+	Negative	Negative	Negative
	liver	+	Negative	Negative	Negative
30	heart	+	Negative	Negative	Negative
	fetal		Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
	mammary		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
35	bladder	+	Negative	Negative	Negative
	adrenal		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
	uterus	Negative	Negative	Negative	Negative
	skeletal		Negative	Negative	Negative
40	muscle	Negative	Negative	Negative	Negative
	PBL	Negative	Negative	Negative	Negative
	placenta	Negative	Negative	Negative	Negative

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spleen	Negative	Negative	Negative	Negative
thymus	Negative	Negative	Negative	Negative
esophagus	Negative	Negative	Negative	Negative

Tumor Tissue

5	renal cancer (4)	+ (2/4)	+ (2/4)	+ (2/4)	+ (2/4)
	colon primary tumors (10)	+ (10/10)	+ (10/10)	+(10/10)	Negative
10	colon mets (4)	+ (4/4)	+ (4/4)	+ (4/4)	Negative
	breast cancer (6)	+ (3/6)	Negative	Negative	Negative
	lung cancer (6)	+ (6/6)	Negative	Negative	Negative
15	gastric cancer (1)	+	+	+	Not tested

colon cancer cell lines

	colo 205	+	+	+	Negative
	HT29	+	+	Negative	Negative
20	HCT15	Negative	Negative	Negative	Negative

**Example 8: Isolation and analysis of additional clones**

For the establishment of a cDNA library from human tissue total RNA was obtained from

25 0.5 g of a renal clear cell carcinoma and established according to the method of Chomzynski as described above. The mRNA was extracted from total RNA with oligo-dT-cellulose. The synthesis of the first strand cDNA was accomplished by the method described by Gubler and Hoffmann, *Gene* 25: 263 (1983) using RNase H and DNA polymerase I. For adaptation of the cDNA Klenow enzyme, adaptors with EcoRI restriction enzyme sites were ligated to the cDNA ends using T4 DNA

30 ligase (Ferretti L and Sgamerella V, *Nucl. Acids Res.* 9: 3695 (1981)). Following restriction enzymatic digestion with the enzyme XhoI, cDNA molecules of different length were separated using Sephacryl 400 and transfected into  $\lambda$ ZAPII phage vectors (Short JM et al., *Nucleic Acids Res.* 16: 7583 (1988)). The recombinant phage DNA was packaged into phages after ligation with packaging extracts and used for the transfection of *E. coli* bacteria. The titration of the library

35 resulted in  $1.8 \times 10^6$  recombinant primary clones. The total cDNA library was transfected in *E. coli* and amplified. The titer of the cDNA library after amplification was  $10^{11}$  plaque forming units per ml (pfu/ml). These transfected cells were used in experiments which follow.



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In accordance with the invention as described above, identification of immunogenic material was achieved by using human sera which has been completely depleted of antibodies directed against antigens derived from native and lytic  $\lambda$  phage-transfected *E. coli* bacteria. To this end, the serum was absorbed, as follows.

5 *E. coli* bacteria of the strain XL1-blue were cultured in 50 ml LB medium overnight. After achieving an optical density of  $OD_{600} = 1.0$ , the bacteria were pelleted by centrifugation, resuspended in 5 ml phosphate buffered saline (PBS), and lysed by sonication. The bacterial lysate was bound onto a matrix of activated Sepharose, which was then put into a column and used for the absorption of the human serum. The serum was run over this column 10 times.

10 A culture of *E. coli* XL1 blue bacteria in the exponential growth phase was pelleted by centrifugation, transfected in 0.01 M magnesium sulfate with  $10^6$   $\lambda$ ZAPII phages without a recombinant insert and incubated in 5 ml LB medium for four hours. The lysate of the transfected bacteria was used in the same manner as the untransfected bacteria, with the human serum described supra being passed through the column an addition ten times.

15 To complete the depletion of the serum, interfering antibodies from lytically transfected *E. coli* bacteria were cultured on agar plates and their proteins were blotted onto nitrocellulose membranes after 10 hours of culture at 37°C. Following this, the serum which had been preabsorbed according to the above steps was transferred to the blotted nitrocellulose membrane, and the absorption procedure was repeated five times. The serum, which was processed in  
20 accordance with the invention, was totally depleted of antibodies directed against antigens derived from *E. coli* and phages.

In this, a renal cancer-specific antigen was identified via the following steps. Bacteria of the strain XL1 blue were transfected with recombinant phages derived from the described cDNA library and plated at a density of  $4 \times 10^3$  plaque forming units (pfu) per plate in LB-medium with  
25 isopropylthiogalactopyranoside ("IPTG"). After 12 hours of incubation at 37°C, nitrocellulose membranes were put on top of the cultures and culture plates were incubated for another four hours. This was followed by incubation of the nitrocellulose membrane for one hour in Tris-buffered saline (PBS) with 5% milk powder. After washing the nitrocellulose membranes three times in TBS, the stripped human serum secured following Example 2 was diluted 1:1000 in TBS/0.5% (w/v) milk  
30 power and incubated overnight with gentle shaking. After the incubation with the nitrocellulose

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membrane the serum was removed and kept for additional testing. Following incubation with serum, the nitrocellulose membranes were washed three times in TBS, and incubated with a polyclonal alkaline phosphatase-conjugated goat anti-human IgG serum for one hour. Following this, the nitrocellulose membranes were washed repeatedly with TBS/0.01% (v/v Tween 20). The reaction was developed using nitroblue tetrazolium chloride and bromochloro-indoyl-phosphate in TBS. The binding of human antibodies to the expressed protein became visible by a blue ring-formed color deposit on the nitro-cellulose membrane. The efficient preabsorption of the serum made it possible to develop the membrane at 37°C over several hours without compromising the quality of the test because of background reactivity caused by antibodies against *E. coli* and phage antigens.

Positive clones were localized on the agar plates, transferred into transfection buffer, and used for a second round of transfection and subcloning. A total of  $1.8 \times 10^6$  recombinant clones were subjected to screening and five different positive-reacting clones were identified.

Positive clones, i.e., those which had bound antibodies derived from the processed human serum, were subcloned to monoclonality by repeated rounds of transfection and testing of reactivity with the processed human serum. P-bluescript phagemids with the respective cDNA inserts were cloned by *in vivo* excision (Hay B and Short JM, *Strategies* 5: 16-19, 1992) from the  $\lambda$ ZAPII phage vectors and used for the transfection of *E. coli* SOLR bacteria. Plasmids were isolated from the bacteria after alkaline lysis with NaOH in a modification of the method of Birnboim HC and Doly J. *J. Nucl. Acids Res.* 7: 1513 (1979). The recombinant plasmid DNA was sequenced according to standard methods using M13-forward and M13-reverse oligonucleotides. The DNA sequence obtained and the resulting amino acid sequence were compared with nucleic acid and protein data banks (Gene Bank, EMBL, Swiss Prot). The sequencing of the cDNA inserts was continued using internal oligonucleotides. Analysis showed no homology with any sequences deposited in the data banks. The full length cDNA clone, referred to as SK313, was cloned with the RACE method (Frohman MA, Dush MK, Martin GR, *Proc. Natl. Acad. Sci. USA* 85: 8998 (1988)), and had a carbonic anhydrase domain at the 5' end.

As a continuation of these experiments, RNA was isolated from a spectrum of malignant and normal human tissues and Northern blots were performed with labeled SK313 (also referred to as clone HOM-RCC-313). The Northern blot analysis demonstrated that the mRNA of clone HOM-

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RCC-313 was overexpressed in 4 out of 19 renal cell carcinomas compared to normal kidneys. Very weak expression was found only in colonic mucosal tissue and in normal kidney. Expression in other tissues was not observed.

To determine the incidence of antibodies against antigens which are identified above,  
5 allogeneic sera from healthy individuals and tumor patients were analyzed. To this end, the sera were processed as described above and depleted from antibodies against antigens derived from *E. coli* and phages. For the detection of antigen-specific antibodies, phages derived from reactive clones were mixed with non-reactive phages derived from the same cDNA library at a ratio of 1:10 and tested as described above for reactivity with antibodies in the human test serum. The serum  
10 which had been used for the identification of the antigen was used as a positive control. The non-reactive phages served as a negative control. A serum sample was positive for antigen reactive antibodies, if the expected percentage of the phage plaques showed a positive reaction. In the case of the renal cell carcinoma antigen represented by clone HOM-RCC-313, the analysis of a spectrum of human sera showed that only sera from renal cell carcinoma patients contained reactive  
15 antibodies. Sera from healthy controls and patients with other tumors did not contain such antibodies.

The cDNA for clone HOM-RCC-313 was excised from the plasmid DNA by digestion with the restriction enzyme EcoR1, was separated by agarose gel electrophoresis, followed by extraction from the gel. This was then used to create a vector which expresses a fusion protein with the  
20 bacterial protein anthranilate synthetase. A relevant fragment in the exact open reading frame was cloned into pATH plasmid vectors (Koerner et al., *Meth. Enzymol.* 194: 477 (1991)). Induction of protein expression was obtained after transformation of the plasmids into *E. coli* of strain BL21 as described (Spindler et al., *J. Virol.* 49: 132 (1984)). Expressed fusion proteins were separated by SDS gel electrophoresis, excised from the gel, eluted and freeze dried. Rabbits were immunized by  
25 subcutaneous injection with 100 µg of the lyophilisate combined with Freund's adjuvant according to standard procedures. Immunization was repeated three times at two-week intervals using incomplete Freund's adjuvant. The rabbit was bled and antiserum was obtained. The obtained antiserum was depleted from antibodies reactive with *E. coli* and phages as described above and tested for reactivity against the renal carcinoma antigen as described for the human serum.  
30 Reactivity was detected at dilutions of 1: >100,000.

Additional clones were identified from pancreatic cancer tumor specimen using the SEREX method of Sahin et al., (1995). A cDNA library was prepared and reacted with high titer IgG in sera of pancreatic carcinoma patients. A total of  $8 \times 10^5$  clones were screened with autologous serum, and  $4.5 \times 10^3$  clones were screened with three different allogeneic sera. Twenty three clones, representing  
5 seven different transcripts were found. Four were previously unknown, unisolated genes. Of the remaining three, glycolytic enzyme aldolase A was found (SEQ ID Nos:799 and 800). Another molecule was "known" in that it was homologous to the rat eIF-5 gene (SEQ ID Nos:801 and 802), which is a eukaryotic translation initiation factor. The human eIF-5 gene was not previously known.

When hepatocellular carcinoma libraries were studied in the same way, a total of  $1.5 \times 10^6$   
10 clones were screened, and 98 positives were found. A total of 59 of these were sequenced, and corresponded to at least 20 different transcripts. Nine of these were assayed with allogeneic sera from hepatocellular cancer (HCC) patients and normal patients. High titered antibody was restricted to HCC patients. The majority of isolated sequences did not correspond to known molecules. Three which did were human albumin (SEQ ID Nos:803 and 804), senescence marker protein SMP30  
15 (SEQ ID NOs:805 and 806), and C3VS (SEQ ID NOs:807 and 808). The latter was overexpressed in 2 of 4 hepatocarcinoma tissues, as compared to normal. Expression of SMP30 was found to vary highly.

The methodology was combined with subtractive cDNA techniques when assaying leukemia cells (T-ALL). An antigen was found which was identical to a broadly expressed, DNA repair  
20 enzyme.

Further assays identified the known molecule galectin-9 (SEQ ID NOs:809 and 810), as being highly expressed on human macrophages and dendritic cells. Expression is upregulated during differentiation of monocytes to macrophages. Highest levels were found on monocyte derived, dendritic cells.

25 Fusion proteins "LD1-mFc" and "LD2-mFc" were constructed to help analyze galectin-9. These consist of murine IgG heavy chain fragments, and a lectin domain (LD1, or LD2), as the N-terminus. Analysis indicated that the C-terminal lectin domain binds to the surface ligands, while the cell surface ligands recognized by the C-terminal lectin domain of galactin-9 was expressed only in a small, subpopulation of dendritic cells.

30 Further analysis of ovarian cancer cells (500,000 clones, using the SEREX method described

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above), identified previously known antigens MAGE-4 (SEQ ID Nos:811 and 812) and restin (SEQ ID Nos:813 and 814), and six other newly identified molecules.

Further experiments were carried out which involved restin. A variation of restin is known, i.e., "CLIP170", which was reported to mediate binding of endosomes to microlubules. It was found that both resin and CLIP 170 are highly expressed in dendritic cells, and are involved in the formation and transport of macropinosomes, a feature of professional antigen presenting cells. Expression of restin was induced after 48 hours of culture of monocytes in GM-CSF/IL-4 supplemented medium. Highest levels were found in immature dendritic cells. When microlubile systems, which are essential for the activity of restin/CLIP-170 were disrupted, macropinocytosis was lost completely.

Further work with the methodology disclosed herein on glioma identified a clone encoding nm23-H2 protein (SEQ ID Nos:815 and 816). This clone corresponds to subunit B of nucleoside diphosphate kinase, which is implicated in tumor metastasis control. It is also known as PuF, a transcriptional factor, for c-myc proto-oncogenes. Antibodies against the protein were found in 1 of 18 sera of brain malignancy patients, 3 of 20 melanoma patients, and 2 of 20 sera from healthy patients. When expression studies were carried out using RT-PCR, 25 of 28 brain tumor, and 4 or 5 meningioma tumor samples were found to express the gene.

#### **Example 9: Isolation and analysis of lung cancer clones**

A cDNA library was constructed from a case of moderately differentiated adenocarcinoma of the lung, obtained from the Department of Pathology at The New York Hospital. The library was constructed in a  $\lambda$ ZAP Express vector using a cDNA library kit (Stratagene, La Jolla, CA).

The cDNA library was screened with autologous patient's serum as described previously [Sahin, U. et al., *Proc Natl Acad Sci USA* 92:11810-3 (1995); Chen, Y.T. et al. *Proc Natl Acad Sci USA*. 94:1914-8 (1997)]. Briefly, the serum was diluted 1:10, pre-absorbed with transfected *E. coli* lysate, and a 1:10 dilution of the absorbed serum (final dilution of serum 1:100) was incubated overnight at room temperature with the nitrocellulose membranes containing the phage plaques. After washing, the filters were incubated with alkaline phosphatase-conjugated goat anti-human Fc  $\gamma$  secondary antibodies and the reactive phage plaques were visualized by incubating with 5-bromo-4-chloro-3-indolyl-phosphate and nitroblue tetrazolium. Phagemid clones encoding human

immunoglobulin sequences were subsequently eliminated during the secondary screening.

The reactive clones were subcloned, purified, and *in vitro* excised to pBK-CMV plasmid forms (Stratagene). Plasmid DNA was prepared using Wizard Miniprep DNA Purification System (Promega, Madison, WI). The inserted DNA was evaluated by EcoRI-XbaI restriction mapping, and clones representing different cDNA inserts were sequenced. The sequencing reactions were performed by DNA Services at Cornell University (Ithaca, NY) using ABI PRISM (Perkin Elmer) automated sequencers.

To evaluate the mRNA expression pattern of the cloned cDNA in normal and malignant tissues, gene-specific oligonucleotide primers for PCR were designed to amplify cDNA segments of 300-400bp in length, with the estimated primer melting temperature in the range of 65-70°C. All primers were commercially synthesized (Operon Technologies, Alameda, CA). RT-PCR were performed using 35 amplification cycles in a thermal cycler (Perkin Elmer) at an annealing temperature of 60°C.

Genomic DNA were extracted from cell lines and frozen tumor tissue. Following restriction enzyme digestion, the DNA was separated on a 0.7% agarose gel, blotted onto nitrocellulose filters, and hybridized to an a <sup>32</sup>P-labeled DNA probe at high stringency (65°C, aqueous buffer). Washing of the blot was also under high stringency conditions, with a final wash in 0.2XSSC with 0.2% SDS at 65°C.

To identify the 5' end of the mRNA transcripts, RACE (rapid amplification of cDNA ends) methodology was utilized using the Marathon cDNA amplification kit (Clontech) and adaptor-ligated testicular cDNA as the substrate. The PCR products, after separation by agarose gel electrophoresis, were cloned into the direct PCR cloning vector pGEM-T (Promega).

Single-strand conformation polymorphism (SSCP) analysis was performed to analyze cDNA from various tissues, using previously described protocols [Drapoli, C.D. et al., New York: John Wiley and Sons, Inc. (1997)]. Briefly, PCR was performed with 5 µl RT product in a final volume of 25 µl, with 2µCi of α<sup>32</sup>P-dCTP (~3000 Ci/mmol, New England Nuclear) per reaction. The PCR conditions was as described for RT-PCR above. After the PCR, 1 µl of the mixture was diluted with 5 µl of denaturing buffer (95% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanol), heat-denatured at 98°C for 2 min, and electrophoresed through an 8% polyacrylamide gel with 10% glycerol. As controls, aliquots of the same samples were diluted with a standard non-

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denaturing DNA loading dye and electrophoresed in parallel. The electrophoresis was performed at room temperature at a constant power of 10-12 watts. The gel was then dried and autoradiography performed for 15-24 hours with an intensifying screen.

#### 5 Identification of Immunoreactive cDNA clones

A cDNA expression library of  $1.42 \times 10^7$  primary clones was prepared from Lu15, a specimen of moderately differentiated adenocarcinoma of the lung and  $8 \times 10^5$  phage plaques were immunoscreened with absorbed autologous patient serum at 1:100 dilution. Excluding false-positive clones encoding immunoglobulin gene fragments, 20 positive clones were identified. These clones were purified and sequence analyzed. Comparisons of the sequences showed that these clones represented cDNAs from 12 distinct genes, designated NY-LU-1 through NY-LU-12 (Table 9). A homology search through the GenBank/EMBO databases revealed that 4 of the 12 genes corresponded to previously known molecules, and 8 others were unknown genes, with sequence identity limited only to short segments of known genes or to expressed sequence tags (ESTs).

Table 9: NY-LU clones

Gene Designation	Gene/Sequence Identity [Accession Number]	cDNA	Comments
NY-LU-1	Aldolase A (N and H type) [X06352]	Lu-15/24, 72, 83, 158, 219, 241	Human fructose, 1,6 diphosphate aldolase A. Expressed in muscle (M type), but also in most other tissues (N and H types). Levels increased in most lung cancers; released into blood upon trauma and in several cancers.
NY-LU-2	hASNA-1 [U60276]	Lu-15/26, 66	Human homolog of the ATP-binding ars A component of the bacterial arsenite transporter. Previously cloned by SEREX from a testicular library (Chen et al., unpolished). Ubiquitously expressed.
NY-LU-3	Annexin 1X [L19605]	LU-15/64	Homosapiens 56K autoantigen. Antibodies to Annexin 1X are found in multiple autoimmune diseases. ubiquitously expressed.

NY-LU-4	Rip-1 [U55766]	Lu-15/65	Human HIV Rev-interacting protein. Expressed in B cells, monocytes and rhabdomyoma cells.
NY-LU-5	Unknown [W61291, W92962, etc.]	Lu-15/80	Expressed ubiquitously (by RT-PCR).
NY-LU-6	Unknown [none]	Lu-15/85	Sequence contains no ORF, expressed ubiquitously (by RT-PCR).
NY-LU-7	Unknown [W23466, AA167732, etc.]	Lu-15/135,217	Expressed in neuron, pregnant uterus, lung ca., parathyroid tumors, etc.
NY-LU-8	Unknown [Z78323, N39225, etc.]	Lu-15/139	Expressed in fetal heart, retin, multiple sclerosis, etc.
NY-LU-9	Unknown [W26569, AA036884, etc.]	Lu-15/145	Expressed in retina, pregnant uterus, fetal liver-spleen, etc.
NY-LU-10	Unknown [M29204, etc.]	Lu-15/154	Expressed in colon, pancreas, pregnant uterus, fibroblasts, etc.
NY-LU-11	Unknown [W23466, AA057400, etc.]	Lu-15/270	Expressed in retina, pregnant uterus, fetal heart, fetal liver-spleen, parathyroid tumors, etc.
NY-LU-12	g16	Lu-15/251	Located at the 3p21 TSG locus (see text)

Of the 4 known genes, aldolase A (NY-LU-1; SEQ ID NOs:689 and 690) was most frequently isolated, representing 6 of 20 primary positive clones in the entire screening. NY-LU-2 (SEQ ID NO:691), represented by two isolates, was the human homolog of the ATP-binding *arsA* component of the bacterial arsenite transporter, a gene which has been shown to be ubiquitously expressed in various tissues [Kurdi-Haidar, B. et al., *Genomics* 36:486-91 (1996)]. NY-LU-3 (SEQ ID Nos:692 and 693) encodes annexin XI, which is a 56KD ubiquitously expressed antigen to which autoantibodies have been described in sera from patients with various autoimmune diseases [Misaki, Y. et al., *J Biol Chem* 269:4240-6 (1994); Misaki, Y. et al., *J Rheumatol.* 22:97-102 (1995)]. The last gene in this group, NY-LU-4 (SEQ ID NOs:694 and 695), codes for the human HIV Rev interacting protein Rip-1, which has been shown to be expressed in the monocyte cell line U937, the rhabdomyoma cell line RD, as well as in adherent monocytes and primary lymphocytes [Refaeli, Y.



et al., *Proc Natl Acad Sci USA* 92:3621-5 (1995)].

Of the eight unknown genes, 6 (NY-LU-5, 7, 8, 9, 10, 11; SEQ ID Nos:696, 698, 699, 700, 701 and 702/703, respectively) shared sequence identity with reported expressed sequence tags (EST), likely representing cDNA products derived from the same genes. These ESTs were derived from various somatic tissues unrelated to lung, e.g., neuron, pregnant uterus, colon, endothelial cells, etc., suggesting that these genes are widely expressed in human tissues (Table 9), making them unlikely candidates for vaccine-based tumor immunotherapy. These clones were not further investigated. The only novel gene in this group, NY-LU-6 (SEQ ID NO:697), showed no sequence identity to deposited sequences in the public databases. The tissue expression pattern of this gene was evaluated by RT-PCR analysis using gene-specific primers and a normal tissue RNA panel consisting of lung, colon, kidney, liver, brain and testis. Results showed universal expression in these tissues, and this clone was not further analyzed.

NY-LU-12 is on TSG locus of chromosome 3p21.

The last gene in the unknown gene group, NY-LU-12, was represented by the immunoreactive clone Lu15-251. This clone, 1081bp in length, contained an uninterrupted open reading frame (ORF) of 952 bp, followed by a 129bp 3'untranslated region. No translation initiation codon was identified, indicating that this was a partial cDNA clone.

A sequence homology search revealed that this gene shared up to 30% homology with two different human proteins at its C-terminus (Fig. 1), LUCA15 and DXS8237E (GenBank accession numbers U23946, and P98175) and also shared homology to S1-1, the rat counterpart of DXS8237E [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)]. LUCA15 was subsequently proven to be a gene immediately centromeric to NY-LU-12 on the TSG locus on chromosome 3p21 (see below and [Wei, M.H. et al., *Cancer Res.* 56: 2487-92 (1996)]). Our analysis of LUCA15 revealed the presence of a nuclear localization signal in the putative LUCA15 protein. DXS8237E, was located on chromosome Xp11.23 [Coleman, M.P. et al., *Genomics* 31:135-8 (1996)] and its rat homolog, S1-1, has been shown to be an RNA-binding protein [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)].

Of particular interest, however, was that a short segment (92bp) at the 5' end of NY-LU-12 was identical to a previously identified gene, g16 (GenBank accession number U50839), which was

mapped to chromosome 3p21.3 and was interrupted in the small cell lung cancer line NCI-H740.

To compare NY-LU-12 with g16, the full-length NY-LU-12 cDNA sequence was obtained from normal testicular mRNA through a combination of 5'RACE and direct PCR cloning strategies.

The predominant cDNA form (SEQ ID No:707), excluding the poly A tail, is of 3591bp in length.

5 An open-reading-frame of 1123 amino acid residues (SEQ ID No:708) was identified (nt. 102-3470), with 101bp of 5' untranslated and 129bp of the 3' untranslated region. The nucleotide and amino acid sequences are shown in Fig. 2.

Comparison with the g16 sequence verified that these two are identical genes and mapped NY-LU-12 to *TSG* locus on 3p21. However, the reported g16 sequence, 2433 bp in length, lacks the  
10 5' end 110 bases which include the translational initiation codon at nucleotide 102, and also the 3' end 980 nucleotides of NY-LU-12. In addition, 74bp DNA segment (nt. 1587-1659 of NY-LU-12) was absent in the reported g16 sequence. Oligonucleotide primers flanking this 74 bp region were designed and used to amplify RNA from 1 normal lung, 5 lung cancer cell lines, and 6 lung cancer specimens. Two RT-PCR products were seen in every specimen, corresponding to the sizes of the  
15 two cDNA variants. It was thus concluded that this variation represents an alternate splicing event which occurs in both normal and cancerous lung tissues. Of interest, however, was the difference in the putative translational products resulting from this additional 74bp exon. In the absence of this exon, the open-reading-frame of NY-LU-12 would end in the termination codon at nt.1736, as reported for g16, with a total length of 520 amino acid residues (in contrast to 1123 residues in the  
20 longer transcript). Moreover, this shorter form would not encode the C-terminal portion of the NY-LU-12 protein, the segment responsible for the immunoreactivity of Lu15-251 to the autologous patient serum.

#### Additional cDNA variants of NY-LU-12

25 In the process of 5'RACE cloning of the full-length NY-LU-12, three minor forms of cDNA products were identified which varied in their transcriptional initiation site and in their exon usage in the 5' segment of this gene. These variants will be described as transcripts B, C, and D (SEQ ID Nos:709, 711 and 712). Fig. 3 shows the comparison of these transcripts to the predominant cDNA form (transcript A, see Fig. 2).

30 Transcript B (Fig. 3A, bottom) contains an additional exon of 208 base pairs, inserted at

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nucleotide 145 of the NY-LU-12 sequence. The original ORF of NY-LU-12 is disrupted due to this inserted sequence, and the AUG initiation codon used by transcript A is thus unlikely to be used by this transcript. A new potential translational initiation site, however, is found within this new exon and would continue the translation into the ORF of transcript A. The final product would be a protein of 1177 amino acids (SEQ ID NO:710), with the 69 residues at the N-terminus different from transcript A. Interestingly, this new exon encodes for a signal peptide not present in the transcript A (Fig. 3A, bottom), and it is possible that these two products are localized to different subcellular compartments.

Similar to transcript B, transcripts C and D both contained additional exon(s) not present in transcript A. Transcript C contained two extra exons in tandem and a length of 364bp, only one of which (137bp) was present in transcript D, Figure 3B. These extra exon(s), inserted at the same alternate splicing site as transcript B, disrupted the original ORF, and the only long ORF would initiate at nucleotide position 498 of NY-LU-12 (959 of transcript C, 635 of transcript D). Considering the long untranslated region at the 5' end, it is doubtful whether transcripts C and D are indeed translated *in vivo*.

Correlating with this variation of NY-LU-12 mRNA, Northern blot analysis showed several RNA species in normal tissues, ranging approximately from 3 to 4.4 Kb. The intensity of individual bands also appear to vary among different tissues, suggesting post-transcriptional tissue specific regulation of NY-LU-12 mRNA.

#### Features of NY-LU-12 and its putative gene product

Analysis of the NY-LU-12 amino acid sequence showed 20 inexact 6 amino acid repeats with a consensus sequence of D(F/Y)RGR(D/E) close to the N-terminus (Fig. 2). These repeats were separated by 4 to 6 amino acid intervals, which showed no apparent sequence homology among each other. This feature in primary sequence is distinctive among known proteins. Hydrophilicity plot revealed that this region, although hydrophilic in general, has regular hydrophobic turns, and these cycles of hydrophilicity changes correspond to the hexapeptide repeats. Although the significance of this characteristic is unclear at present, this segment of sequence is highly rich in arginine and aspartic acid, a feature shared by RNA binding proteins. Similar motifs, rich in arginine and aspartic acid residues, were found in other RNA-binding proteins [Witte, M.M.

et al., *Proc Natl Acad Sci USA* 94: 1212-7 (1997); Wilson, R. et al., *Nature* 368:32-8 (1994); Seraphin, B. et al., *Nature* 337:84-7 (1989); Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], e.g., RNA [Seraphin, B. et al., *Nature* 337:84-7 (1989)] hnRNA 3' end cleavage stimulation factor [Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], etc., indicating that NY-LU-12 is likely to be an RNA-binding protein. Consistent with this, PROSITE analysis of the putative NY-LU-12 protein identified a bipartite nuclear localization signal between amino acids 1016-1032 and a 4-residue nuclear localization pattern (PRKR) at amino acid 604-607 (Fig. 2), suggesting that NY-LU-12 is a nuclear protein. Analysis for post-translational modification sites showed potential sites for tyrosine sulfation, amidation, as well as phosphorylation sites for protein kinase A, C, casein kinase II, and tyrosine kinase. A PEST region, peptide sequences consistently found among unstable proteins with short half lives, was identified at amino acids 897-928 (Fig. 2), implying NY-LU-12 as an unstable protein.

#### Southern blot analysis of NY-LU-12 in normal and tumor tissues

To investigate the status of NY-LU-12 in normal and tumor cells, Southern blot analysis was performed on 9 lung cancer cell lines (3 adenocarcinoma, 2 squamous, and 3 large cell anaplastic), Lu15 tumor DNA, and a colon cancer cell line HT29 (Fig. 4). (HT29 was included due to the finding of an EST identified in the GenBank, accession number AA079461, which appeared to be a fusion sequence between semaphorin IV gene and NY-LU-12.) Using a 1.1Kb cDNA probe (nucleotide 1095-2140) and HindIII digested DNA, the results showed that one of the two hybridizing bands was absent in NCI-H740, confirming that NY-LU-12 was partially deleted in this cell line. The breakpoint of this deletion, by using primers from different regions, was further defined to be between nucleotides 1433 and 1777 of NY-LU-12, with the 3' sequences homozygously deleted. Besides NCI-H740, however, no evidence of homozygous deletion was seen in any other tumor cell line sample or in LU15. The similar band intensities and identical sizes of the DNA signals in all specimens also argued against the possibility of a heterozygous deletion or translocation of this gene, at least in the region analyzed. No change was found in HT29, suggesting that the semaphorin IV/NY-LU-12 fusion sequence in the GenBank probably represents a cloning artifact.

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SSCP and sequence analysis of NY-LU-12 in Lu15 tumor DNA.

The mapping of NY-LU-12 to the lung cancer *TSG* locus raised the possibility that an altered protein product due to mutational event may be the basis for the autologous immune recognition. This possibility was explored using DNA sequencing and single-strand confirmational polymorphism (SSCP) analysis.

The DNA sequence contained in the immunoreactive clone Lu15-251 (nucleotide 2518-3599 of NY-LU-12) was obtained from the normal counterpart by RT-PCR cloning using autologous normal lung tissue, and no mutations were found when compared to Lu15-251.

RT-PCR SSCP was then used to analyze the entire NY-LU-12 gene, comparing Lu15 tumor tissue and autologous normal lung tissue. To encompass the whole sequence, 10 sets of primer pairs were designed, each amplifying a range of 205 to 603 bps. For products >400bps, a restriction enzyme digestion step was added prior to the electrophoresis step to further reduce the fragment sizes and increase the assay sensitivity. Results showed no reproducible changes between normal and tumor tissues, and thus no evidence of mutation in Lu15 tumor cDNA. A representative set of SSCP analysis is shown in Fig. 5.

Serological response to NY-LU-12 in lung cancer patient

The frequency of anti-NY-LU-12 response was examined among normal adult and patient sera using the phage plaque assay identical to the original immunoscreening procedure. Of 21 absorbed sera from allogeneic lung cancer patients, one (Lu22) reacted strongly with the Lu15-251 plaque at 1:1000 dilution, and another (Lu7) also reacted at 1:1000, but only weakly. Nineteen other lung cancer patient sera were non-reactive, nor were the sera from 16 healthy donors, 15 colon cancer, 5 breast cancer, 1 renal cancer, 1 prostate cancer, 1 esophageal cancer, and 1 melanoma patients.

Example 10: Expression analysis of additional cancer associated nucleic acids

The clone RING 3 was isolated from breast SEREX analysis as LONY-Br-5 (see above). The gene was identified as homologous to the "bromodomain testis" gene (BRDT; GenBank accession number AF019085). Analysis of related genes identified BRDT as a gene expressed only in testis, which was then investigated by RT-PCR analysis as described above.

The primers used to perform RT-PCR had the following sequences:

BRDT F1: CAAGAAAGGCACTCAACAG (bp 543-563 of BRDT)

BRDT R1: TTCACTACTTGCTTTAACTGC (bp 776-797 of BRDT)

The meiotic protein H1T (Histone 1 Testis; GenBank accession number M60094) was

5 identified through a literature search for meiotic proteins (testis specific expression).

The primers used to perform RT-PCR had the following sequences:

H1F1: TGCCGAACCTCTCTGTGTC (bp 116-135 of H1T)

H1R1: GCTTCGTGTAGATTTAGGAATC (bp 344-366 of H1T)

10 Table 10: RT-PCR analysis

	<u>Normal Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	mammary gland	-	-
	liver	-	-
15	small intestine	-	-
	brain	-	+/- (very weak)
	lung	-	-
	fetal brain	-	-
	placenta	+	+
20	kidney	-	-
	skeletal muscle	-	-
	pancreas	-	-
	adrenal gland	-	-
	heart	-	-
25	thymus	-	-
	uterus	-	-
	prostate	-	+/- (very weak)
	spleen	-	-
	Testis	+	+

	<u>Tumor Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	Colon	0/6	0/6
35	Breast	0/6	6/6+
	Melanoma	0/12	3/12+
	Lung	8/26+	4/26+
	Renal	0/2	0/2
	Ovary	0/2	0/2
40	Esophageal	0/1	0/1

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Gastric	0/1	0/1
Bladder	0/2	0/2

Lung cancer specific expression of BRDT was observed (see table above). BRDT was expressed only in normal testis and possibly in placenta. The expression analysis of HIT revealed that all breast tumor samples (6 of 6) and ~30% lung cancers and melanoma tissue samples expressed HIT. HIT was expressed in normal testis and possibly in placenta and brain.

### **Example 11: allogeneic serotyping**

To confirm the cancer associated expression of SEREX clones, allogenic sera screening of gastric cancer patients' sera was conducted. Sera from normal patients (gastritis) was used as a control for expression of the clones in non-gastric cancer. The screening procedure used was as described above for the SEREX screening, except for the absorption of anti-bacterial and anti-bacteriophage antibodies. The modifications were as follows.

Serum from a stomach cancer patient or a normal individual was diluted to 1:10 in TBS (Tris buffered saline; final volume 5 ml) and passed through a column (BIO-RAD Poly-Prep Chromatography Column, Hercules, CA, USA) containing 0.5 ml Sepharose-4B cross linked to E. coli Y1090 lysate and 0.5 ml Sepharose-4B cross linked to E. coli BNN97 (5 Prime 3 Prime, Inc, Boulder, CO, USA). After repeating the column chromatography 10 times, serum was then diluted to 1:100 in TBS containing 1% BSA and 0.02% sodium azide. To remove antibodies to bacteria and bacteriophages further, 10 ml absorbed serum was incubated overnight with a 82 mm nitrocellulose membrane on which XL-1 Blue MRF' bacteria and lambda ZAP Express phages (Stratagene, La Jolla, CA USA) were immobilized. The serum was stored at - 80°C until use. For allogeneic typing, an equal numbers of positive phage and negative phage were mixed and plated and processed by the standard SEREX screening procedure.

The results of the allogenic screening experiments follow:

**Table 11: Allogenic Sera Screening of SEREX Sequences from Gastric Patients**

Sequence		Isolated in Serex Patients	Allogenic Serotyping Gastric Cancer Sera	Allogenic Serotyping Normal Sera
Gene/Clone	Number			
RPB-J H-2K binding factor		SM1	6/12	6/16
5 Telomeric repeat binding protein		SM1	1/12	0/16
Ser/Thr protein kinase		SM1	1/12	0/16
SRY interacting protein-1		SM1	2/12	1/16
Sterol carrier protein X		SM1	2/12	0/16
10 Archain		SM1	1/12	1/16
HEM-1		SM1	2/12	1/16
Id-1 helix-loop-helix protein		SM1	1/12	0/16
15 helix-loop-helix transcription factor		SM1	1/12	0/16
Follistatin related precursor protein		SM1,CK, KM	6/12	0/16
Translation initiation factor eIF-4gamma		SM1,SS1, KM	5/12	2/16
20 M phase phosphoprotein 1		SM1,SS1	8/12	5/16
Lysal tRNA synthase		SM1	1/12	0/16
Gelsolin		SM1	4/12	0/16
Zinc finger protein		SM1	1/12	1/16
Goliath		SM1	2/12	1/16
25 zhx-1		SM1	1/12	1/16
SG24		SM1,SS1, KM	5/12	0/16
SG132		SM1	3/12	0/16
S553		SM1	7/12	7/16
S134		SM1	3/12	0/16
30 S328		SM1	2/12	1/16
S365		SM1, KM	2/12	0/16



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	FKBP25		KM, SS1	5/12	0/16
	Pros-27		KM, CK	3/12	1/16
	BS4		KM	1/12	1/16
	GnRH-II		KM	1/12	0/16
5	CTBP		KM	1/12	0/16
	ETF		KM	3/12	1/16
	KIAA0438		KM	1/12	5/16
	KIAA0367		KM	4/12	3/16
	APK1		KM	2/12	0/16
10	IPP		KM	1/12	0/16
	Tropomyosin		KM	1/12	0/16
	p63		KM	1/12	0/16
	KIAA0181		KM	1/12	0/16
	KIAA0349		KM	1/12	0/16
15	RPB1		KM	5/12	9/15
	PPIM		KM	1/12	-
	EB virus		KM	3/12	-
	G.KM073		KM	6/12	-
	G.KM403		KM	1/12	-
20	KM192		KM	1/12	-
	KM294		KM	1/12	-
	KM362		KM	1/12	-
	KM031		KM	1/12	-
	KM081		KM	3/12	-
25	KM201		KM	1/12	-
	KM1496		KM	1/12	-
	KM334		KM	1/12	-
	KM313		KM	1/12	-
	E-cad/Y		CK	1/12	0/16
30	IPBP		SS1	1/4	-
	OS-9		SS1	1/4	-

Kinesin light chain		SS1	1/4	-
---------------------	--	-----	-----	---

The screening results shown above confirm the association of the SEREX clones with cancer. There is a higher correlation of cancer and the expression of certain clones, in particular, follistatin related precursor protein, the translation initiation factor eIF-4gamma, the unknown sequence SG24, the FK506-binding protein 25, and the unknown sequence G.KM073. These clones are well suited to serve as diagnostic indicators of disease and as targets for therapeutics (e.g., vaccine compositions) development.

#### 10 **Example 12: Preparation of recombinant cancer associated antigens**

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. In one method, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells. Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, e.g. certain breast cancer and gastric cancer associated antigens, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

#### **Example 13: Preparation of antibodies to cancer associated antigens**

The recombinant cancer associated antigens produced as in Example 12 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated

antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

**Example 14: Expression of cancer associated antigens in cancers of similar and different origin.**

The expression of one or more of the cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic serotyping using a modified SEREX protocol (as described above for gastric clones).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

**Example 15: HLA typing of patients positive for cancer associated antigen**

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient and typed for HLA class I or class II, as

well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

**Example 16: Characterization of breast cancer associated antigen peptides presented by MHC class I and class II molecules.**

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described in Example 15, the HLA types which present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (see, e.g., Parker et al., *J. Immunol.* 152:163, 1994; D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL <http://bimas.dcrt.nih.gov>. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpfennig (PCT/US96/03182)).

The lung cancer SEREX clone polypeptides NY-LU-12 and NY-LU-12B (variant B), SEQ ID NOs: 708 and 710, were subjected to the HLA binding peptide analysis described above, using the NIH website, to identify HLA binding peptides for several common HLA molecules (HLA-A1, A2, A3, A24, B7, B44, and B52). The results are listed below in Table 12.

Table 12: Identification of HLA binding peptides in lung SEREX clones

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		amino acids of		
HLA	peptide	NY-LU-12 protein	SEQ ID NO	
5	A1	NVEE-HSFSY	67 - 75	713
		PVDP-NILDY	287 - 295	714
		DTDY-RSMEY	398 - 406	715
10	A2	SLLE-DAIGC	506 - 514	716
		TLMI-QDKEV	521 - 529	717
		YVSSLDFWYC	533 - 542	718
		VIVEVLEPYV	671 - 680	719
		KLTD-WNKLA	948 - 956	720
		QLSDLHKQNL	975 - 984	721
		KQSEQELAYL	991 - 1000	722
		KLVDKEDIDT	1042 - 1051	723
15		VMFA-RYKEL	1114 - 1122	724
20	A3	QMFG-YGQSK	417 - 425	725
		GMPVKNLQLK	481 - 490	726
		GLPE-EEEIK	823 - 831	727
		LLCRRQFPNK	958 - 967	728
25	A24	EYRD-VDHRL	405 - 413	729
		GYVC-VEFSL	499 - 507	730
		DYGY-VCVEF	497 - 505	731
		WYCKRCKANI	540 - 549	732
		TYPQPQKTSI	574 - 583	733
		IYRSTPPEVI	663 - 672	734
		HYYQ-GKKYF	754 - 762	735
		VYVP-QDPGL	816 - 824	736
30	B7	WNRDYPPPPL	26 - 35	737
		MPPV-DPNIL	285 - 293	738
		TARD-AQRDL	432 - 440	739
		GPSEEKPSRL	448 - 457	740
		TPPEVIVEVL	667 - 676	741
35		RVMFARYKEL	1113 - 1122	742
40	B44	REMG-SCMEF	272 - 280	743
		EEQSSDAGLF	376 - 385	744
		KEYN-TGYDY	490 - 498	745
		TEAKQELITY	566 - 575	746
		VEALRVVKIL	710 - 719	747
		GEYG-GDSYD	906 - 914	748
		LERREREGKF	1000 - 1009	749

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B52	RQDGESKTIM	650 - 659	750
	TPPEVIVEVL	667 - 676	751
	YGFIDLDSHV	701 - 710	752
	RQFP-NKEVL	962 - 970	753

5

## NY-LU-12B (variant B)

A1	NVEE-HSFSY	121 - 129	754	
10	PVDP-NILDY	341 - 349	755	
	DTDY-RSMEY	452 - 460	756	
A2	WQSA-RFYYL	41 - 49	757	
	SLLE-DAIGC	560 - 568	758	
15	TLMI-QDKEV	575 - 583	759	
	YVSSLDWFYC	587 - 596	760	
	VIVEVLEPYV	725 - 734	761	
	KLTD-WNKLA	1002 - 1010	762	
	QLSDLHKQNL	1029 - 1038	763	
20	KQSEQELAYL	1045 - 1054	764	
	KLVDKEDIDT	1096 - 1105	765	
	VMFA-RYKEL	1168 - 1176	766	
A3	QMFG-YGQSK	471 - 479	767	
25	GMPVKNLQLK	535 - 544	768	
	GLPE-EEEIK	877 - 885	769	
	LLCRRQFPNK	1012 - 1021	770	
A24	YYLN-ATDVL	47 - 55	771	
30	FYYLNATDVL	46 - 55	772	
	EYRD-VDHRL	459 - 467	773	
	GYVC-VEFSL	553 - 561	774	
	DYGY-VCVEF	551 - 559	775	
	WYCKRCKANI	594 - 603	776	
35	TYPQPQKTSI	628 - 637	777	
	IYRSTPPEVI	717 - 726	778	
	HYYQ-GKKYF	808 - 816	779	
	VYVP-QDPGL	870 - 878	780	
40	B7	WNRDYP P P P L	80 - 89	781
		MPPV-DPNIL	339 - 347	782
		TARD-AQRDL	486 - 494	783
		GPSEEKPSRL	502 - 511	784
		TPPEVIVEVL	721 - 730	785
45		RVMFARYKEL	1167 - 1176	786

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5	B44	SEAWSSNEKF	59 - 68	787
		REMG-SCMEF	326 - 334	788
		EEQSSDAGLF	430 - 439	789
		KEYN-TGYDY	544 - 552	790
		TEAKQELITY	620 - 629	791
		VEALRVVKIL	764 - 773	792
		GEYG-GDSY	960 - 968	793
		LERREREGKF	1054 - 1063	794
10	B52	RQDGESKTIM	704 - 713	795
		TPPEVIVEVL	721 - 730	796
		YGFIDLDSHV	755 - 764	797
		RQFP-NKEVL	1016 - 1024	798

15 Likewise, other clones identified herein can be analyzed for the presence of candidate HLA binding peptides using no more than routine experimentation.

#### **Example 17: Identification of the portion of a cancer associated polypeptide encoding an antigen**

20 To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching

25 the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (*see, e.g., Knuth et al., Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.* 24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230,

30 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by <sup>51</sup>Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by

exonuclease III digestion or other standard molecular biology methods. Synthetic peptides are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or  $^{51}\text{Cr}$  release as above.

5 Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

10 A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by CTLs. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

15

#### EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

20

All references disclosed herein are incorporated by reference in their entirety.

We claim:



## TABLE 1

## SEQ ID NO. 1:

5 U72994, AC004022, Z68323, AE001160, L34078, AF064863, AC002132, U60440, X66494, N21242, AA678312, W86762, R01605, AA782843, AA275156, W41927, AA874648, AA571241, AA562747, W10480, AA451301, AA866631, AA466667, AA999057, AI029140.

## 10 SEQ ID NO. 2:

AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648, AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648.

## 15 SEQ ID NO. 3:

X98371, AL009008, L31790, Z83220, X92946, AC003975, AF008916, U80460, X75544, X66732, X95275, X52177, X07976, AC004451, Z74307, AB000878, AL009179, AF038667, 20 Z78544, Z48008, U23486, J05096, AB000882, Z30213, L11593, U18530, L27325, AC005191, M99579, AA130270, AA158245, AA903098, AI018453, AA436455, AA980593, AA172479, AA637487, AA116588, AA426854, AA050404, AA390025, AI006618, AI048382, C85944, AA673480, AI006510, AA823338, AA413694, W35075, AA015033, AA413584, W29693, AA637069, AA619839, AA125149, AA039004, AA674696, AA871138, AA414747, 25 AA198099, C91478, F071359, AA925957, AA820054, H16496, AI043756, AA892435, AA893551, AA818669, AA892785, AA944026, D33919, N96570, F19798, AI045451, AA800662, D65187, AA944025, AA925731, AA892314, AA945449.

## 30 SEQ ID NO. 4:

AA900930, AA925665.

## 35 SEQ ID NO. 5:

U58105, Z81485, Z54236, Z48584, U61375, M55267, M59856, X51942, U77302, Z48621, AF032455, Z11866, AB013392, L32792, AA871997, AA084083, AA130829, AA083063, AA666290, N38894, D54459, T28921, AA806015, AA512059, AI043087, AI042894, 40 AA968324, AA238493, AA237462, AI042885, AI046424, AI035670, AA269430, AA250621, AI035540, AA260613, AA106870, AA238658, AA106134, AI042683, AA105958, AA144007, AA986558, AA457910, AA389400, AA673056, AA153254, AA754678, AI021109, AA390813, C36687, T41571, AI011183, AI013356, AI011739, AI030260, AA924384, C44421.

## 45 SEQ ID NO. 6:

AF036717, U91327, AF036718, U56248, Z48795, U99290, AI30697, U58204, M24417, AF022983, M33581, AC004619, H64641, AA477478, AA369676, AA088359, AA057574.

AA683066, AA446279, AA332363, T09328, R80982, AA069486, AA410842, C18527,  
AA293033, H12730, AA287344, AA029631, R83063, AA061290, AA185993, AA880204,  
AA499308, AA183172, AA242360, AA792388, AA175587, AA277140, AA880395,  
AA899046, AA859550, C35363, C35702, C32682, F14140, T18049, C83149, T45787,  
5 AA924623, D47525, Z30723, AA897884, AA042465, AI009871, AA875198, C83016.

## SEQ ID NO. 7:

10 X74116, AL022148, AC004548, AC000352, Z11664, Z78065, Z74028, AE000163, AE000750,  
X74229, D90700, R59414, AA176708, W02568, AA354664, R43017, AA973553, F10008,  
D61827, AA826300, Z41398, T77572, R40189, H85823, W86541, T17276, AA679337,  
X83357, AA184845, AA416260, AA475603, AA388692, AA764445, AA388689, AA219880,  
AA290020, AA388507, AA387267, C86741, AA414436, AA451259, AA413796, AA930916,  
15 AA793690, AA619447, AA062257, AA522026, AA816247, AA892032, AA817702, H33461,  
AA925507, AA849449, AI029236, AA247069, AA697975, AA882508, AA893258, AA698410,  
AA891755, AA698227, AA892782, AA899328, T04373, AA567522, AA698408, AA202615,  
AA141016, AA697974, AA697998, C61176, D69691, AI030205, AA586054.

20

## SEQ ID NO. 8:

U08218, L38909, Y11095, AC002431, Z23069, S77418, U39060, L38580, AF053367, Z36506,  
M18102, J03624, AA102264, AA730686, H47968, AA357170, AA130974, C06054,  
25 AA626429, F00559, AA604528, AA383348, AA040127, N84965, D54884, D54883, R94309,  
AA373184, AA128091, W68194, H58283, R76347, AA343938, AA305144, AI049611,  
AA384516, AA720553, N57395, R97387, D52674, AA169408, H66293, AA456362, T74258,  
AA730145, AA101952, N86388, AA355003, AA307640, AA385679, AA354542, N99075,  
N83528, H87678, R84494, R35720, AA670111, AA186452, W32370, D55392, W05161,  
30 AA641280, AA120503, C77063, AA146393, AA620177, AA509478, C77481, AA427148,  
AA474531, W83304, AA207424, AA763436, AA958473, AA799243, AA493061, AA967792,  
AA145256, AA089338, AA756259, AA789767, AA980112, AA866640, AA914516,  
AA821675, AA466770, AA015387, AA816036, AA246546, AA941789, AA955779,  
AA997768, AA997534, T43805, AA956150, T18836, T23333, AA525666, T18787, AA800483,  
35 C64685, AA851367, C91730, AA143899, T23399.

## SEQ ID NO. 9:

40 AP000056, U43491, Z74919, L81498, Z94054, AC002503, L81499, AA740188, AA630241,  
AA974724, AA806907, N88859, N98242, H12649, R06485, R06511, AA546258, C76846,  
AA208416, AA959219, AA276381, W10055, AA462844, AA444278, W13447, W97802,  
AA542324, AA137880, AA269331, AA175695, W59029, AA003372, AA146233, AI045761,  
C93154, C94084, C94208, D68027, C12780, AA687005, AA080598, C12876, C12390,  
45 AA848674, AA924440, T15031, AA451569, H35524.

## SEQ ID NO. 10:

U25640, AA127328, H24207, H08275, AA283063, AA826096, AA417382, AA464874, W05562, AA453370, N51211, AA495859, R33871, H00927, AA623997, AA220442, AA178568, AA605493, AA394557, AA956116, AA999037, AA818246.

5

SEQ ID NO. 11:

AB001740, AF039956, AA581972, AA594539, AA236870, AA464410, AA237069, AA694199, AI038896, AA167314, AA577381, AA430117, N23143, R53610, W37647, 10 AA724229, AA313202, AA860618, W16866, AA134966, AA255556, AA305224, R50528, AA844913, W32042, W37383, AA908394, W93357, W31353, R55254, N79251, AA456077, AA477700, AA477701, AA989005, AA455580, N32722, N22935, R50622, AA135047, R51941, T34020, T30416, T32309, AA883332, W93445, AA166984, AA026749, T08224, AA255572, W03768, AA033670, W31880, AA772832, AA230974, AA511207, W82274, 15 AA230365, AA671085, AA511230, AA606681, AA023735, AA444535, W98518, W14718, W85455, AA980318, AA137525, AA035840, AA692158, AA007919, W48013, AA444534, AA981497, AA002566, W48089, W99869, AA960396, AA960580, AA145259, AA145683, AA388960, AA389941, AA266272, AA145124, AA267212, AA959753, AA407991, AA175818, AA943997, AA899476, AA899756, AA943998, AA955446, AA012783, AA924956, 20 AA892219, AA955331, AI012225, AA891436.

SEQ ID NO. 12:

25 U72994, AC004022, AF043493, U43252, U43251, U81830, U58105, U68242, Z93242, AL009029, M29872, U12980, M81118, M30471, Z56258, AF012943, AC004080, AC002563, AF024533, AF002991, Z63771, AP000042, AF064863, U80017, AC004087, Z55235, L05920, AA508139, N90748, AA450240, AA948158, AA828938, AA165115, AI003312, AA436633, AA419100, AA743442, AA961990, AA885286, AA861312, T84801, AI040166, AA494115, 30 AA652324, AA181105, AA095541, R59256, AA503712, AA700364, AA603821, T60326, AA779097, AI023884, AA603785, H79111, W39526, AA506607, W94361, N66078, R01605, H22694, W86762, W99303, AA745640, AA678312, AA431870, W41927, AA874648, C92734, C23102, C53080, C91168, D65098, C32959, C50029, M80125, C34452, C83862, C24659, T21473, AA874720, C06696, W43071, AI043300, C53907.

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SEQ ID NO. 13:

X94232, U90437, AC003052, U59809, AC004001, M95396, Z67884, X77486, U70051, 40 X14805, AF022976, Z83823, X77485, J04171, AF036007, U05768, U88315, Z98048, AF036009, AC005179, U41277, U32517, AE001138, D64060, M84387, H29022, AA814221, N26314, AA935912, AA873506, AA608576, AA453605, AA232674, Z38725, AA772022, AA025212, AA318330, R48115, AA234084, H18508, N64543, AA970508, R36933, AA306944, H49559, AA325555, H85834, H89988, AA343974, AA648643, H65664, T62713, 45 H16554, N21122, AA351037, AA484621, AA221492, AA259314, C76383, C76336, AA607924, C76394, AA408562, AA921258, AI006352, W41405, AA153317, AA015435, AA027405, AA794066, AA498038, AA184222, AI011068, AA859614, AA899776, AA955080, AA799674, AA849652, AI009788, AA900928, AI007950, AA109392, AA753592, U92780, AA957632, AA567950, AI009495.

## SEQ ID NO. 14:

AC000075, U66140, R14195, AA220229, T31199, R19104, R19148, Z46126, AA417619,  
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## 10 SEQ ID NO. 15:

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15 AA620556, AA085733, AA187157, AI031865, AA972318, AA897169, W79046, AA531124,  
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## SEQ ID NO. 16:

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## 40 SEQ ID NO. 17:

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45 AB011800, M77194, AE000021, L07268, AE000936, U03115, AF009663, AA582128,  
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## SEQ ID NO. 18:

35 U14003, AE000500, X66784, AF030178, U77066, M10122, M69106, X58072, Z99113, AF004104, AF004101, X55037, X78560, AC004595, X55122, AA481578, AA280143, AA481271, AA280144, AA736516, N79995, R82883, AA355987, AA571000, AA572293, AA738653, AA620225, AA855746, AA563168, AA530645, W40812, AA690944, AA839456, X61848, AA525648, AA141861, AA944854, C94212, AA394778, C83861, H76642, 40 AA559379, AA943112.

## SEQ ID NO. 19:

45 AE000500, AF030178, X66784, Z49405, M69106, M27174, X55037, AF004104, X78560, U51281, L17405, M10122, AC003106, X55122, X05553, AC002368, AF004101, U77066, U77456, X58072, AA481578, AA280143, AA481271, AA280144, AA736516, AA780050, AA359089, R82883, AA355987, AA571000, AA563168, AA738653, AA620225, AA855746, AA572293, AA530645, W40812, AA690944, AA839456, X61848, AA525648, AA944854.

AA141861, C83861, AA943112, AA957703, H76642, C94212, AA394778.

SEQ ID NO. 20:

5 Z99496, AC004518, AC004219, Z70204, J03925, Z66494, AC003053, U40072, AC002980,  
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10 AA242009, AA272568, AA009230, AA880181, AA265864, AA124746, AA801108,  
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SEQ ID NO. 21:

15 U20864, AL021246, AA430998, AA050776, AA104086, AA414390, AA920944, AA624117,  
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SEQ ID NO. 22:

20 Z81462, AF029308, AC004069, AL010265, AL023828, AC004026, AF076274, U96110,  
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SEQ ID NO. 23:

30 X60469, AC000394, L08048, X12597, D63874, U51677, S71186, D43920, U59897, AF026132,  
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35 AF039845, L06147, M60052, X56007, Y00500, X77934, U26708, AL022333, AL021710,  
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## SEQ ID NO. 24:

30 Z93928, U13881, U70475, X89811, X81456, U20532, X04724, J00748, M25585, J04807,  
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40 AA498683, AI046409, C85159, Z84147, AA893230, C06683, C06682, C06639, C06625,  
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## SEQ ID NO. 25:

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## SEQ ID NO. 26:

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## 35 SEQ ID NO. 28:

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5 SEQ ID NO. 29:

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SEQ ID NO. 30:

25 AL022394, Z54200, U12024, AF025391, S73606, L08068, U01053, AP000046, AA282633, H83341, AA744757, AA047741, AA975917, W45279, W90155, W79733, H01158, N47513, AA688093, AA865203, W90027, AA595381, AA054203, AA478596, AA100549, T80668, AI049820, AA047691, AA969720, AA086374, AA159414, W39756, AA159315, H83695, 30 AA909221, T06258, AA969838, AA013361, H05751, H05858, AA665540, D12197, H01159, AA933811, D12219, AA282525, C05204, N47512, R57383, F18424, D79284, W92778, H18813, H20386, N77238, R84635, AA204675, R80129, W95005, T85150, AA523436, AA743656, T84782, W95004, R55724, AA572180, AA790119, W96964, AA420091, AA169954, AA623914, AA623971, AA681631, H32698, AA735717, AF026318.

35

SEQ ID NO. 31:

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SEQ ID NO. 32:

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20 S51033, U58090, AB002777, X71980, AB015609, U25846, U55848, Y14339, AB002533,  
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## SEQ ID NO. 33:

10 U10079, U22176, Z97192, X86553, D16432, Z68908, X98417, X97752, AC005176, AC004235, AA211771, AA019927, AA621920, R49915, AA436746, D81089, F07201, AA279576, R61642, AA363761, N90952, AA351423, W85802, AA827923, N41673, AA452942, AA252094, W95240, AA188552, T99151, T53177, AA223851, AA677535,  
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## 20 SEQ ID NO. 34:

AF041845, U48436, AF012624, L76569, AF025020, AF060179, U51281, Z37092, L12249, D83476, AF017434, AF062008, Z97198, AP000046, AA367417, AA852175, W67669, AA303139, AA243251, AA896193, AA881167, AA989888, AA683969, W62376, AA250652,  
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## SEQ ID NO. 35:

30 AF069301, D17030, D17201, S80107, M15888, U09205, J00127, J00128, M64982, L11356, M58569, AE001140, D10667, M77812, AF001548, U39850, AA188052, W28824, AA380387, AA393863, AA426250, F00243, AA157205, R00525, AA137720, AA244463, AA118832, W97106, AA674322, AA645183, AI020701, AI019310, AA717623, W48327, AA153061,  
35 AA103723, AA800548, T46478, AA751512, C10724, C60506, AA819627.

## SEQ ID NO. 36:

40 U81160, U35246, U66865, AF036234, Z71178, R52780, AA336715, AA337057, R12336, AA296712, AA291962, AA336501, AA387806, AI020063, AA109010, AA867718, AA606883, C11880, AA698152, D65730, AA851373, AI028830, AA941242.

## 45 SEQ ID NO. 37:

## SEQ ID NO. 38:

Z46933, AC003957, X64346, U18759, L31881, U18761, J04123, X79489, U18760, AB012234, U11280, Z35865, AC002461, AC004780, AL008980, Z79601, U23404, Z74859, D89119, AC000387, M76665, Z48149, AA948725, AA226732, AA232882, AA232883, AA767922, W39443, N40268, W06854, AA337266, AA319281, T08800, AA094683, AA151630, T33776, 5 AA151682, AA384011, R21292, AA806313, AA047744, AA411384, H41338, H49115, H50377, C89065, AA221399, AA163971, Z36313, AA120075, W64578, AA673947, AA285838, AA607874, AA798884, C86947, W62715, AA790168, AI037229, AI036718, AA920062, AA866467, Z30824, AA610965, AA907958, AA495425, W43775, C41467, C20235, C20223, C19643, C20439, C68506, C73712, C20236, AA978809, M89274, D74720, 10 AA712627, D74758, C19867, AA816719.

## SEQ ID NO. 39:

15 L41560, Z66499, AC003970, AE001177, AF051320, K02212, D88539, U35665, L41069, Z38118, AA744773, W67994, AA046574, AA130298, N71111, R77986, H61835, AA134115, AA722572, N51491, Z36854, H61836, AA458506, AA459607, AA862531, W68186, AA046661, AA459381, R77891, R60953, AA733213, W05472, AA442998, AA136770, AA127983, AA229166, AA741465, AA003716, AA204457, W34842, AA097555, AA674958, 20 AA770799, W81850, AA623806, C78185, AA002533, AI030850, D26771, AA924818, AA848998, AA923967, AI045386, H32633, AA956916, D86678, T14138, AA925473.

## SEQ ID NO. 40:

25 AB002307, X06289, Y00222, U59322, U28964, X61754, AJ004801, U13913, X79339, AA164880, R02386, AA219744, AA324396, D82199, AA113090, AA305260, AA171458, R59748, R35620, AA326344, AA227875, AA366276, H29212, AA505691, R78747, AA406622, AA020232, W64555, AA450476, W44167, AA049918, W64627, R75474, 30 AA517492, AA612452, AA711884, AA212469, AI048148, AI046831, AA671392, AA855606, AA016843, AA031134, AA208052, AA619148, W34918, AA851114, AA901667, AA054812, AI001233, AA955131, AA943821, AI008608, C72506, AI001373, AI001376, D25096, D21962, AA997901, AA824936, AA998885, AA824820, AA998125, AA859586.

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## SEQ ID NO. 89:

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## SEQ ID NO. 91:

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## 30 SEQ ID NO. 93:

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## SEQ ID NO. 95:

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## SEQ ID NO. 97:

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SEQ ID NO. 101:

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SEQ ID NO. 103:

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SEQ ID NO. 105:

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## SEQ ID NO. 107:

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## SEQ ID NO. 109:

M86752, AF039202, Y15068, U27830, X79770, U89984, AP000020, AL008628, U72207,  
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## SEQ ID NO. 111:

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## SEQ ID NO. 113:

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SEQ ID NO. 115:

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SEQ ID NO. 117:

D13627, Z37164, D42052, Z37163, M97562, Z22289.

SEQ ID NO. 119:

Y08915, AF000577, L31652, AJ223156.

SEQ ID NO. 121:

X91141, X77723, D86066, U70777, D85844, AB001750, Y08613, D38038.

SEQ ID NO. 123:

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SEQ ID NO. 125:

U63333, AF035625, AF055320, AF032984.

SEQ ID NO. 127:

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SEQ ID NO. 129:

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SEQ ID NO. 131:

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SEQ ID NO. 133:

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SEQ ID NO. 135:

AC005175, L12168, M98474, U94696, M88485, Z95972, Z81557, S54909, U59831, 20 AB002387, U59832, AC004221, AC003993, AA505656, AI004052, AA975150, AA904315, R39951, AA908198, AA348001, AA348002, R39437, R39435, D21034, AA365146, AA813999, F12674, AA226122, T50818, AA143492, AA337395, AA003016, AA475640, W78672, AA517530, W45934, AA915424, W54264, AA168145, W11712, D34652, U92753, Z84127, U92730, AA438286, AA978864, AA941236, F14527, D47303, D15953, AA202003, 25 AA979012, AA440964, AA736036, AA246888, AA940864.

SEQ ID NO. 137:

30 AF064604, L63543, AE000647, AF064804, AA443401, AA334624, H69413, H69440, H69851, AA167818, AA830102, N64831, AA947764, AA453748, AA453830, R52194, T30970, AA903211, T32140, T30969, W05727, AA024651, C18655, AA386236, T69012, AA442992, AA452775, AA292522, AA223531, AA221067, AA004165, AA538370, AA067626, AA104327, AA874150, AA450950, AA692789, AA798137, AA119093, AA240418, 35 AA542585, AA520648, AA519835, AI045289, AA520246, AA849945, T75681, AA520090, AA651385, Z25578, AA585901, AA395446, C90090, AA713116, AA851675.

SEQ ID NO. 139:

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M24603, X02596, Y00661, M15025, X06418, U07000, X52829, M19730, M30829, X52831, M30832, X14676, X52828, X52830, S72479, L02935, M64437, M17542, L19704, U01147, X07537, X14677, X14675, M17541, M17543, M19695, X76485, AF023460, X89600, U19759, AF039083, X71790, AC004679, AC002076, AF035456, M99565, Z72005, Z79997, AL021154, 45 Z98259, AC003108, L13706, AF018254, M69197, U67228, Z75887, U14661, M84472, AC005200, AC001228, AC004761, Z95124, AC002540, Z79699, AE000926, U43572, U51281, D82351, AB013379, U34879, AC002425, AC004598, AA338585, AA333142, AA126116, H55543, H55721, R54267, H55614, H55699, H55545, AA744741, AA772917, H29052, AA573543, T16608, AA773472, AA775416, AA601919, AA470534, AA351521,

AI015318, AA351163, AA486365, AA470985, AA565376, AA344993, R92629, AA553555, AA740903,  
AA090392, H94289, AA457592, AI033503, T69709, R94066, AA040853, AA065296,  
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AA802030, C74658, AA246925, AA803435, C27952, AA944566, AA817514, C83561,  
AA978443, C24959, C82705, C72516, H34014, AA712916, AA820781, D21893, D15866.

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SEQ ID NO. 141:

S45630, AF007162, X95383, AF029793, M55534, X60351, S77138, S77142, S74229, X60352,  
M63170, M24906, M28638, J03849, M12016, M73741, U04320, M12014, M24092, L08078,  
15 S53164, U26661, M12015, M25770, U16124, X87114, D29960, X14789, X85205, M17247,  
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AA482745, AA211607, N28898.

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SEQ ID NO. 143:

U78082, L78810, U14573, AC004068, U07561, M98511, AC004673, AA613346, AA953216,  
AA305926, H92800, R98218, AA629543, AA297666, AA302982, AA429481, AA126005,  
25 AA837225, AA856961, AA946848, F13749, AA847704, AA833896, AA621381, AA833875,  
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AI028510, AA483606, AA992126, T54783, AA715075, AA568204, AA715173, N64587,  
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AA663472, AA490602, AA857673, AA347114, AI049630, AA086150, AI017251, AA877992,  
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AA610233, AA654874, AA501867, AA604831, N22058, AA492114, T50676, AA757426,  
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AA159978, AA534204.

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SEQ ID NO. 145:

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L76702.

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SEQ ID NO. 147:

L07872, L34544, L34543, X17459, S63463, M81871, L08904, U60093, U60094, L07873,  
L07874.

SEQ ID NO. 149:

U07158, X85784, AJ000541, U76832, L20821, AC003089, AC004504, AF049236, L40609,  
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5 AA732931, AA610556, AA973899, AA598896, AA531553, AA826535, AI000209, AA290836,  
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AA833281, AA619252, C77541, AA691960, AA763615, AA164051, AA259589, AA060475,  
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10  
SEQ ID NO. 151:

M13451, X03445, X03444, M13452, X66870, X76297, X14170, X99257, D14850, D13181,  
L12399.

15  
SEQ ID NO. 153:

U28918, U17714, X82021, Z98048, D17265, D17092, Z82022, L04270.

20  
SEQ ID NO. 155:

X54859, Z86000, AC003043, X77738, X77737, L35930, AC003084, AC000111, M89651,  
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L78442, U00921, AC004692, AC003698, AE000742, Z49128, Z73417, Z71418, AA424638,  
AA442084, AA805748, AA835489, AA713576, AA502343, AA765949, AA812332,  
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30 AA904521, AA372550, R48898, N50390, R08712, H83343, AA417867, AA090407,  
AA009846, AA927286, AA678135, AI033148, AI041408, AA235113, AA398662, M62215,  
W27276, AA885767, AA460155, AA742433, R19908, AA040696, AA555240, AA043160,  
AA292844, R53160, AA536080, N70013, N35921, N70096, AA277029, AA560610,  
AI046716, AA237153, W15784, AA547132, AA231089, AA170968, D46090, C61892,  
35 C64408, D34777, D35175, D35914, D37381, AA559708, D37143, C60784, AI008855,  
AI021808, AI009216, D68214, AA220863, D70434.

40  
SEQ ID NO. 157:

U43195, U58512, U61266, D89493, U36909.

45  
SEQ ID NO. 159:

AF069442, AF001295, M13820, M10081, AB010077, AA491075, AA446881, AA588390,  
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AA882303, AA791693, AA822133, AI037224, AA404165, AI036575, AA499662, AA864136,  
AA561223, AA183703, AA647218, AA792208, W48100, D40621, AJ225487, AA294595.

02866, H35041, AA944944, AA597316, D26977, D68334, AA685934, W88345, AA964819.

## SEQ ID NO. 161:

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K01546, AE000468, X95549, AC004014, Z81584, L19201, X94244, X06932, U39479, X13301, AC000386, U80847, X86737, U39478, AA883211, AA610050, AA774254, AA280736, AA926725, AA459300, N55370, AA233666, H90342, T66839, H91250, AA856968, R92873, AI034196, AI014787, AA910410, AA088535, AA230765, AA467238, 10 AA397279, AA420226, AA396042, AA200070, AA165873, AA762534, AA067133, AA065429, AA185092, AA572057, AA111387, AA175824, AA881071, AA571692, AA104279, AA733670, AI008804, D86670, C67200, D41938, AA141467, D35894, AI001643, AA957220, T37355, T18792, D47809, W21723, AA898504, AA951903, AA661025, AA949796, AA990685, AA661449, AA948837, R04787, D16046, AA439636, AA246769, 15 AA978829, D43523, T02021, AA803212, D22651, AA201227, AA694728, AA891643, D23309, AA820831, D41871, W21774, D16065.

## SEQ ID NO. 163:

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X15183, AF028832, D87666, J04633, L33676, X07270, U94395, M27024, M30627, X16857, X07265, M36830, M30626, AA669137, AA725103, AA890496, AA314095, AA554815, AA313331, AA730100, AA214035, AA876412, AA121630, AA314010, AA927532, AA968674, AA679253, N66271, AA558907, AA309988, AA587079, AA075436, AA160964, 25 AA205657, AA214083, AA130903, AA917032, AA149623, AA857523, AA889843, AA305037, AA491055, W73240, AA255644, W73295, AA765431, AA178947, N66409, AA074895, AA306976, AA075052, AA075387, AA130892, AA857443, AA405942, AA629891, AA152004, AA129550, W56527, AA513807, AA703828, AA223171, C75280, AA889155, AA854676, AA773063, AA774999, AA152392, AA307057, AA316954, 30 AA657352, AA522607, AA188113, AA026444, AI003623, AA312717, AA312400, T64299, AA178992, AA228992, AI042136, AA457613, AI032857, AA164461, AA625127, AA807763, AA130815, AA054695, AA937097, W93534, N67875, AA526896, W52802, AA527942, N34251, W28646, AA668543, AA496091, W52511, AA070581, AA306826, AA120908, AA699607, AA086423, N72134, AA630369, AA564649, AA046806, AA666249, AA306893, 35 AA225404, AA127417, AA854951.

## SEQ ID NO. 165:

M23885, AF047868, AF017732, AB005249, Z83229, AF026483, U97194, Z67884, Z67881, X13481, X07651, AC001226, AC002542, AB002307, AA984684, AA017533, AA306600, AA261957, F08123, R17885, AA282208, H85861, H85836, AA593150, H87276, AA057384, AA243602, AA013399, AA374926, AA721341, R88896, AA021538, AA101740, AA375314, AA090398, H86058, AA984556, AA215816, AA092672, AA034243, AA328017, F11174, 45 AA261777, N40306, W21253, R02386, AA349225, AI038487, H98027, AA385878, AA075431, AA375596, R77638, T73214, AA310841, AA062331, AA919318, AA606883, 373 AA174568, AA790426, AA423321, AA647673, AA109549, AA396473, W16215, AA105538, AA061105, AA066766, AA462773, AA555644, AA499452, AA389523, AA245036, AA475340, AA880992, AA198965, W11981, AA509705, AA237414, AA646230, AA673569.

AA239037, AA672620, AA915168, AA863498, AA123378.

SEQ ID NO. 167:

5

Y11251, AF030234, AF043945, L40407.

SEQ ID NO. 169:

10

U33822, X61838, AA572230, AA589570, AA929790, AA104830, C81582, AA271190,  
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15

SEQ ID NO. 170:

D32050, D16969, AC004423, S81497.

20

SEQ ID NO. 172:

D86982, L07131, M14544, AA296228, AA318436, AA296234, H88394, W26642, AF038251,  
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25 AA122437, AA277698, W75741, AI036117, AA980469, AA033178, AI006694, AA980625,  
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AA217057, AI045760, R64866, D40836, D41873, AA509279, D40089, AA114361, AA751642,  
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D40199, AA958134, AA072494, AI008727, AA618978, AA848687, C21884, AA113662,  
30 AA945653, AA660093, C58446, AA908068, AA532100, AA264560, AA426658, AA097169,  
AA751535.

SEQ ID NO. 174:

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Z81364, AC003033, AE000665, AA570483, AA532739, AA526905, AA725306, AA134415,  
AA651838, AA481316, AA600310, C04532, AA004615, H20713, AA913640.

40 \_SEQ ID NO: 176

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45 L37107, AF060514, S77819, X13058, D86070, U50395, U07182, U90328, Y08900, M75144,  
Y08901, U74487, U48619, K01700, M13872, AF051368, U48616, U48618, X00741, M13874,  
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K02110, U59757, M22895, M13118, U63714, M22888, M13116, M22894, M13117, U51857,  
U37120, U62133, U07020, X91793, L07907, U26741, U59758, S78456, L23634, U22145.



X00879, X00881, S77930, S78457, U66066, D63399, U44835, L07908, S57234, D63405, L27630, M22896, U07019, D63404, M13119, X13057, D63402, M75145, D63401, L12046, AA373960, H61357, AA358870, AA928725, H90357, AA302363, R94782, W24142, AA448185, AA004394, AA376121, AA151197, W76037, R82621, AA157426, AA343323, 5 AA301677, AA002978, AA966981, AA839925, AA982800, AA030090, D77246, AA184043, AA142337, AA529242, AA874521, AA048636, AA168688, AA032325, AA881664, AA529082, AA874036, W06121, AA520602, R86591, AA848372, D37535, AA433405, C72790, AI009692, C25990, X91325, D71516.

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SEQ ID NO: 177

X71973, AC004151, L24896, X82679, AF045769, AF045768, U37427, D87896, S80257, L12743, X76009, X76008, AF035264, AC004707, AA633971, AA588533, AA992915, 15 AA399565, AA435883, AA454856, AA877822, AA780281, AA767205, AI016009, AI038211, AA417004, AA400522, AA676416, AA526712, AA431710, AA496292, AI041168, AA451858, AA709014, AA588291, AA758304, AA188597, AA149890, AA815107, AA670145, AA026421, AA468719, R67030, AI024175, AA719171, AA708025, W15350, AA431760, AA887242, AA888171, AA769788, AA948489, N54495, AA453278, AA887529, AI014760, 20 AA287946, AA862377, H44827, W72726, N22715, AA662838, AA187825, AA780142, N70623, AA503741, AA024544, AI023537, AA834970, AA062885, AA991970, AA576623, AA722713, AI014758, AA765436, AA633498, AA507435, C01757, N70601, AA314727, R62311, AI004483, R81700, W60860, AA621104, H51422, N33007, AA046316, H20797, R70369, AA724141, AA694532, H20024, AA627821, AA448392, H93528, AI015880, 25 AA453376, AA977808, AA576363, AA838346, N78626, AA648742, AA305364, H20123, AA024543, AA864931, AA946666, AA417190, W73759, AA815325, AA128171, AA809918, AI039304, AA718260, AA088979, AA403403, W85396, AA222552, AA839828, AA071896, AA109679, AA470211, AA219887, AA816136, W83835, AA064566, AA606943, AA034666, AA270485, AA457957, AA571899, AA050132, AA510431, AI020265, AA590096, W97284, 30 AA691964, W78537, W08051, AA435081, AA020097, W15024, AA008493, AA208204, W53741, AA512604, AA049396, W64741, AA756852, AA048836, AA038639, W14765, W10901, AA920385, AA791715, AA647984, AA690893, W75172, AA184727, AA036383, AA275344, AA619559, AA059803, AA575700, AA967063, W83433, AA203908, AA959416, AA222749, W15727, AA684313, AA286343, AA145935, AA137494, AA272180, AA472719, 35 AA208001, AI006169, AA240906, D19204, AA276329, W59005, AA445679, AA510539, AA222929, AA144725, AA413110, AA268012, AA492769, AA545011, AA204126, W17735, AA516923, AA270092, AA518734, AA475396, AA108883, AA014248, AA221781, AA051598, AA667607, AA048854, AA623999, AA397087, AI006246, AA122798, AA675710, AA462388, AA606840, AA516903, AA407638, AA222968, AA064375, C25916, AA941583, 40 C94734, AI011423, AA893085, AA964072, AA957524, AA963336, AA956783, AI014112, AA894190, C20441, AA231739, D68624, AA964536, AT000114, D22968.

SEQ ID NO: 178

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Z50194, U92983, U44088, AC003101, X72892, AF035444, M32474, AF019953, AC001228, Y15443, AF001294, U12418, X06956, M31176, AF015277, AF002708, R43556, AA088367, AA313553, H92530, AA376262, T09403, AA814143, R75643, AA479005, AA773048, AA507143, AA402127, AA430292, AI015600, AA393069, AA463606, AA885498, AA460759.

AA398766, R48359, AA426107, AA909990, AI017459, AA076224, N39533, AI026941,  
AA412699, AA292828, AI024759, AI016910, AA573306, R48386, AA065307, AA774549,  
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5 AA637983, AA020137, AA097337, AA117759, W17615, AA285526, AA111347, AA208823,  
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AI013412, T15040, AA541011, AA990782, AA851306, AA540938, T23386, AA783863,  
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10 D15562, T20348, AA966363, AA949269, AA785774, AA728671, D16092, N37869, D48782.

## SEQ ID NO: 179

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## SEQ ID NO: 180

25 D87072, U52191, L25270, L29564, L29563, D83144, U73169, AC003036, AC003049,  
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30 T03226, AA867674, AA009101, AA726511, W90906, AA028401, W54470, AA266581,  
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AA656978, AA162676, AA051548, AA038373, AA032527, AA840207, AA273185,  
AA260228, AA051553, W56956, D89319, AI045498, D24681, AA801346, AA962980,  
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15 SEQ ID NO: 194

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45 SEQ ID NO: 198

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SEQ ID NO: 201

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5 SEQ ID NO: 263

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SEQ ID NO:264

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35 SEQ ID NO:265

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15 SEQ ID NO: 270

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## SEQ ID NO: 272

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## SEQ ID NO: 274

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## SEQ ID NO: 275

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25 SEQ ID NO: 319

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5 SEQ ID NO: 321

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35 SEQ ID NO: 471

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15 SEQ ID NO: 473

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10 SEQ ID NO: 490

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20 AA240112, AA153656, W82776, AA104976, AA562089, AA396048, AI007191, AA797994,  
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25 SEQ ID NO: 491

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20 SEQ ID NO: 507

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35 SEQ ID NO: 508

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45 SEQ ID NO: 514

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5 SEQ ID NO: 519

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20 SEQ ID NO: 532

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AA425945, AA425945 zv84a12.s1 Soares total fetus Nb2HF8 9w Ho... 595 e-168  
AA436368, AA436368 zv32f05.s1 Soares ovary tumor NbHOT Homo s... 585 e-165  
AA975130, AA975130 on06f01.s1 NCI\_CGAP\_Lei2 Homo sapiens cDNA... 579 e-163  
AA885226, AA885226 am34e06.s1 Soares NFL T GBC S1 Homo sapien... 559 e-157  
AA912472, AA912472 ol96e03.s1 NCI\_CGAP\_PNS1 Homo sapiens cDNA... 555 e-156  
AA320935, AA320935 EST23388 Adipose tissue, white II Homo sap... 553 e-155

AA042872, AA042872 zk56b07.s1 Soares pregnant uterus NbHPU Ho... 543 e-152  
 T08932, T08932 EST06824 Homo sapiens cDNA clone HIBBM46 5' end. 537 e-150  
 AA488258, AA488258 ad08f07.r1 Soares NbHFB Homo sapiens cDNA ... 533 e-149  
 T19350, T19350 h03012t Testis 1 Homo sapiens cDNA clone h0301... 496 e-138  
 H87681, H87681 yw15e04.r1 Homo sapiens cDNA clone 252318 5'. 490 e-136  
 H81522, H81522 yu61h08.r1 Homo sapiens cDNA clone 230655 5'. 466 e-129  
 T49620, T49620 ya77g03.s1 Homo sapiens cDNA clone 67732 3'. 452 e-125  
 R14363, R14363 yf80d10.r1 Homo sapiens cDNA clone 28995 5' si... 446 e-123  
 AA211476, AA211476 zp75h11.s1 Stratagene HeLa cell s3 937216 ... 430 e-118  
 N46636, N46636 yy48a09.r1 Homo sapiens cDNA clone 276760 5'. 424 e-116  
 Z17358, HSDHII065 H. sapiens partial cDNA sequence: clone H1... 416 e-114  
 R40737, R40737 yf80d10.s1 Homo sapiens cDNA clone 28995 3'. 400 e-109  
 AA410278, AA410278 zv32f05.r1 Soares ovary tumor NbHOT Homo s... 383 e-104  
 AA496574, AA496574 zv37b03.s1 Soares ovary tumor NbHOT Homo s... 375 e-101  
 N34907, N34907 yy48a09.s1 Homo sapiens cDNA clone 276760 3'. 371 e-100  
 T49619, T49619 ya77g03.r1 Homo sapiens cDNA clone 67732 5'. 355 1e-95  
 AA301480, AA301480 EST14551 Thymus III Homo sapiens cDNA 5' end 341 2e-91  
 R31593, R31593 yh76f03.s1 Homo sapiens cDNA clone 135677 3'. 317 2e-84  
 AA984591, AA984591 am89d10.s1 Stratagene schizo brain S11 Hom... 313 4e-83  
 AA338831, AA338831 EST43831 Fetal brain I Homo sapiens cDNA 5... 238 2e-60  
 T07305, T07305 EST05194 Homo sapiens cDNA clone HFBEG86. 230 4e-58  
 AA159942, AA159942 zo79c05.r1 Stratagene pancreas (#937208) II... 204 3e-50  
 R57355, R57355 F2878 Fetal heart Homo sapiens cDNA clone F287... 196 6e-48  
 AA729237, AA729237 nx35c08.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 192 1e-46  
 AA877709, AA877709 nr09g11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 172 9e-41  
 AA969195, AA969195 op51c03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 107 4e-21  
 AA327432, AA327432 EST30768 Colon I Homo sapiens cDNA 5' end 80 1e-12  
 AA854147, AA854147 aj71f01.s1 Soares parathyroid tumor NbHPA ... 74 6e-11  
 AA983156, AA983156 oq51g09.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 66 2e-08  
 H09529, H09529 yl95h10.s1 Homo sapiens cDNA clone 46129 3'. 66 2e-08  
 AA286791, AA286791 zs54h07.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 66 2e-08  
 W04418, W04418 za43c06.r1 Soares fetal liver spleen 1NFLS Hom... 58 4e-06  
 AA101045, AA101045 zm27e12.r1 Stratagene pancreas (#937208) H... 56 1e-05  
 AA064706, AA064706 zm13f07.r1 Stratagene pancreas (#937208) H... 42 0.22  
 AA810035, AA810035 od11f12.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.86  
 T41169, T41169 ya31g10.s3 Homo sapiens cDNA clone 62274 3' co... 40 0.86  
 AA070108, AA070108 zm69d06.s1 Stratagene neuroepithelium (#93... 40 0.86  
 AA706183, AA706183 ag93e01.s1 Stratagene hNT neuron (#937233)... 40 0.86  
 AA393069, AA393069 zt69e09.r1 Soares testis NHT Homo sapiens ... 40 0.86  
 AA371600, AA371600 EST83650 Pituitary gland, subtracted (prol... 40 0.86  
 AA977820, AA977820 oq78a09.s1 NCI\_CGAP\_Kid6 Homo sapiens cDNA... 38 3.4  
 AA584760, AA584760 no04c06.s1 NCI\_CGAP\_Phe1 Homo sapiens cDNA... 38 3.4  
 AA584615, AA584615 no08g12.s1 NCI\_CGAP\_Phe1 Homo sapiens cDNA... 38 3.4  
 AA229827, AA229827 nc48c04.r1 NCI\_CGAP\_Pr3 Homo sapiens cDNA ... 38 3.4  
 W21398, W21398 zb50a11.r1 Soares fetal lung NbHL19W Homo sapi... 38 3.4



AA136933, AA136933 zn97f07.sl Stratagene fetal retina 937202 ... 38 3.4

AA869501, AA869501 vq08g11.rl Barstead stromal cell line MPLR... 833 0.0  
 AA221749, AA221749 my28g01.rl Barstead mouse pooled organs MP... 789 0.0  
 AA271363, AA271363 va71d08.rl Soares mouse 3NME12.5 Mus muscu... 781 0.0  
 AA544727, AA544727 vk35d01.rl Soares mouse mammary gland NbMM... 773 0.0  
 W84968, W84968 mf42e02.rl Soares mouse embryo NbME13.5 14.5 M... 640 0.0  
 AA153324, AA153324 ms61e11.rl Stratagene mouse embryonic carc... 617 e-175  
 AA673899, AA673899 vo86g07.rl Barstead mouse irradiated colon... 583 e-164  
 AA797488, AA797488 vw28a05.rl Soares mouse mammary gland NbMM... 519 e-145  
 W71831, W71831 me45b06.rl Soares mouse embryo NbME13.5 14.5 M... 472 e-131  
 AA213358, AA213358 mu74e04.rl Stratagene mouse embryonic carc... 444 e-123  
 W75918, W75918 me82f05.rl Soares mouse embryo NbME13.5 14.5 M... 444 e-123  
 AA038141, AA038141 mi81e05.rl Soares mouse p3NMF19.5 Mus musc... 359 3e-97  
 AA038288, AA038288 mi83b04.rl Soares mouse p3NMF19.5 Mus musc... 323 1e-86  
 AA017742, AA017742 mh40c03.rl Soares mouse placenta 4NbMP13.5... 297 8e-79  
 AA771297, AA771297 vt17g04.rl Barstead mouse myotubes MPLRB5 ... 297 8e-79  
 AA105228, AA105228 mp45b11.rl Barstead MPLRB1 Mus musculus cD... 295 3e-78  
 AA068340, AA068340 mm53f01.rl Stratagene mouse embryonic carc... 293 1e-77  
 AA612347, AA612347 vo05c08.rl Stratagene mouse skin (#937313)... 281 5e-74  
 AA038300, AA038300 mi83d04.rl Soares mouse p3NMF19.5 Mus musc... 270 2e-70  
 AA500952, AA500952 vg01h04.rl Soares mouse NbMH Mus musculus ... 252 4e-65  
 W08368, W08368 mb41f07.rl Soares mouse p3NMF19.5 Mus musculus... 212 4e-53  
 AA052280, AA052280 ma82e12.rl Soares mouse p3NMF19.5 Mus musc... 123 3e-26  
 AA064466, AA064466 ml49c05.rl Stratagene mouse testis (#93730... 107 2e-21  
 AA271566, AA271566 vb74b09.rl Soares mouse 3NME12.5 Mus muscu... 60 3e-07  
 C86222, C86222 Mus musculus fertilized egg cDNA 3'-end sque... 42 0.078  
 W83632, W83632 mf31a04.rl Soares mouse embryo NbME13.5 14.5 M... 42 0.078  
 AA423627, AA423627 ve80f01.rl Soares mouse mammary gland NbMM... 42 0.078  
 AA036586, AA036586 mi41h08.rl Soares mouse embryo NbME13.5 14... 42 0.078  
 AA207496, AA207496 mv78g02.rl GuayWoodford Beier mouse kidney... 42 0.078  
 AA120433, AA120433 mp82h11.rl Soares 2NbMT Mus musculus cDNA ... 42 0.078  
 W08185, W08185 mb42h02.rl Soares mouse p3NMF19.5 Mus musculus... 38 1.2  
 AA065563, AA065563 ml71b06.rl Stratagene mouse kidney (#93731... 38 1.2  
 AA288756, AA288756 mr46h07.rl Life Tech mouse embryo 15 5dpc ... 38 1.2  
 AA119334, AA119334 mp80e10.rl Soares 2NbMT Mus musculus cDNA ... 38 1.2  
 AA163051, AA163051 ms24a10.rl Stratagene mouse skin (#937313)... 38 1.2  
 N28074, N28074 MDB1392R Mouse brain. Stratagene Mus musculus ... 38 1.2  
 AA288757, AA288757 mr46h08.rl Life Tech mouse embryo 15 5dpc ... 38 1.2  
 AA122857, AA122857 mq06a02.rl Soares 2NbMT Mus musculus cDNA ... 38 1.2  
 AA617519, AA617519 vj77d05.rl Knowles Solter mouse blastocyst... 38 1.2

W89420, W89420 mf80b03.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2  
 AI047837, AI047837 ud64c11.x1 Sugano mouse liver mlia Mus mus... 38 1.2  
 AA840310, AA840310 vw91a10.r1 Stratagene mouse skin (#937313)... 36 4.8  
 AA986428, AA986428 ue13b04.x1 Sugano mouse embryo mewa Mus mu... 36 4.8  
 W47677, W47677 mc89g07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA057996, AA057996 mj56c10.r1 Soares mouse embryo NbME13.5 14... 36 4.8  
 AA183858, AA183858 mo95h01.r1 Stratagene mouse testis (#93730... 36 4.8  
 AA212232, AA212232 mu43e08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 W41067, W41067 mc39a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.8  
 AA967594, AA967594 uh01d06.r1 Soares mouse hypothalamus NMHy ... 36 4.8  
 AA414093, AA414093 vc64c07.s1 Knowles Solter mouse 2 cell Mus... 36 4.8  
 AA123833, AA123833 mp93c03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 AA432920, AA432920 vd91b11.r1 Soares mouse NbMH Mus musculus ... 36 4.8  
 AA874496, AA874496 vx03a08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 AA000433, AA000433 me76e09.r1 Soares mouse embryo NbME13.5 14... 36 4.8  
 AA023983, AA023983 mh94a07.r1 Soares mouse placenta 4NbMP13.5... 36 4.8  
 AA013726, AA013726 mh12e09.r1 Soares mouse placenta 4NbMP13.5... 36 4.8  
 AA274648, AA274648 vb08c01.r1 Soares mouse NML Mus musculus c... 36 4.8  
 AA140347, AA140347 mq89g06.r1 Stratagene mouse heart (#937316... 36 4.8  
 AA499377, AA499377 vi89c07.r1 Stratagene mouse heart (#937316... 36 4.8  
 C88747, C88747 Mus musculus early blastocyst cDNA, clone 01B... 36 4.8  
 AA726125, AA726125 vu88c06.r1 Stratagene mouse skin (#937313)... 36 4.8  
 AA760311, AA760311 vv71c12.r1 Stratagene mouse skin (#937313)... 36 4.8  
 AA763007, AA763007 vw60b05.r1 Soares mouse mammary gland NMLM... 36 4.8  
 AA929878, AA929878 vz44d03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 W59064, W59064 md67e10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA103519, AA103519 mo24b12.r1 Life Tech mouse embryo 13 5dpc ... 36 4.8  
 AA222310, AA222310 my14d08.r1 Barstead mouse heart MPLRB3 Mus... 36 4.8  
 W83557, W83557 mf32d02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA168631, AA168631 ms33c05.r1 Stratagene mouse skin (#937313)... 36 4.8  
 AA960143, AA960143 vw60b05.s1 Soares mouse mammary gland NMLM... 36 4.8  
 W34557, W34557 mc58a05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 W98818, W98818 mf94e06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA008527, AA008527 mg85h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8  
 AA008734, AA008734 mg86h03.r1 Soares mouse embryo NbME13.5 14... 36 4.8  
 AA510568, AA510568 vg33a10.r1 Soares mouse mammary gland NbMM... 36 4.8  
 AA672524, AA672524 vo59e11.r1 Soares mouse mammary gland NbMM... 36 4.8  
 AA052773, AA052773 mf24h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8  
 AA096626, AA096626 mo09h06.r1 Life Tech mouse embryo 10 5dpc ... 36 4.8  
 AA124880, AA124880 mp73e06.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 AA198005, AA198005 mv12b09.r1 GuayWoodford Beier mouse kidney... 36 4.8  
 AA624213, AA624213 vm98h06.r1 Knowles Solter mouse blastocyst... 36 4.8  
 AA521863, AA521863 vi08b01.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8  
 AA692113, AA692113 vt19d03.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8  
 W71551, W71551 me39e11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8

AA646501, AA646501	vn12g12.r1 Stratagene mouse heart (#937316...	36	4.8
AA607056, AA607056	vm95e05.r1 Knowles Solter mouse blastocyst...	36	4.8
AA163340, AA163340	ms65b10.r1 Stratagene mouse embryonic carc...	36	4.8
AA110893, AA110893	mm02b04.r1 Stratagene mouse kidney (#93731...	36	4.8
AI030290, AI030290	UI-R-C0-jb-d-01-0-UI.s1 UI-R-C0 Rattus nor...	293	1e-77
C71833, C71833	Rice cDNA, partial sequence (E0428_1A)	44	0.017
AA926551, AA926551	TENS1173 T. cruzi epimastigote normalized ...	42	0.069
AA875699, AA875699	TENU0170 T.cruzi epimastigote normalized c...	42	0.069
AA567661, AA567661	HL01595.5prime HL Drosophila melanogaster ...	40	0.27
C74504, C74504	Rice cDNA, partial sequence (E31753_1A)	40	0.27
AA698333, AA698333	HL04291.5prime HL Drosophila melanogaster ...	38	1.1
AA441429, AA441429	LD16359.5prime LD Drosophila melanogaster ...	38	1.1
N68770, N68770	TgESTzy35b12.r1 TgRH Tachyzoite cDNA Toxoplas...	38	1.1
AA246440, AA246440	LD05311.5prime LD Drosophila melanogaster ...	38	1.1
AA801776, AA801776	GM12975.5prime GM Drosophila melanogaster ...	38	1.1
N69148, N69148	TgESTzy33d10.r1 TgRH Tachyzoite cDNA Toxoplas...	38	1.1
AA536484, AA536484	LD17114.5prime LD Drosophila melanogaster ...	38	1.1
AA392544, AA392544	LD11451.5prime LD Drosophila melanogaster ...	38	1.1
AA202696, AA202696	LD03182.5prime LD Drosophila melanogaster ...	38	1.1
AA392367, AA392367	LD11287.5prime LD Drosophila melanogaster ...	38	1.1
AA264629, AA264629	LD08245.5prime LD Drosophila melanogaster ...	38	1.1
AA735318, AA735318	LD21104.5prime LD Drosophila melanogaster ...	38	1.1
AA264558, AA264558	LD08333.5prime LD Drosophila melanogaster ...	38	1.1
AA536476, AA536476	LD17106.5prime LD Drosophila Embryo Drosop...	38	1.1
AA957774, AA957774	UI-R-E1-fv-f-04-0-UI.s1 UI-R-E1 Rattus nor...	38	1.1
AA567991, AA567991	HL02092.5prime HL Drosophila melanogaster ...	38	1.1
AA957876, AA957876	UI-R-E1-fv-f-04-0-UI.s2 UI-R-E1 Rattus nor...	38	1.1
AA892488, AA892488	EST196291 Normalized rat kidney, Bento Soa...	38	1.1
AA699001, AA699001	HL06668.5prime HL Drosophila melanogaster ...	36	4.3
C19706, C19706	Rice cDNA, partial sequence (E10809_1A)	36	4.3
D41773, RICS4574A	Rice cDNA, partial sequence (S4574_2A).	36	4.3
C40680, C40680	C.elegans cDNA clone yk247c4 : 5' end. single...	36	4.3
AA698625, AA698625	HL05354.5prime HL Drosophila melanogaster ...	36	4.3
C82819, C82819	Oryctolagus cuniculus corneal endothelial cDN...	36	4.3
D46016, RICS10393A	Rice cDNA, partial sequence (S10393_3A).	36	4.3
AA536314, AA536314	LD16858.5prime LD Drosophila melanogaster ...	36	4.3
AA801012, AA801012	EST190509 Normalized rat muscle, Bento Soa...	36	4.3
D46541, RICS11289A	Rice cDNA, partial sequence (S11289_1A).	36	4.3
D47315, RICS12612A	Rice cDNA, partial sequence (S12612_1A).	36	4.3
AA735857, AA735857	GM09977.5prime GM Drosophila melanogaster ...	36	4.3
AA753921, AA753921	97BS0370 Rice Immature Seed Lambda ZAPH c...	36	4.3
D47243, RICS12505A	Rice cDNA, partial sequence (S12505_1A).	36	4.3
AA978395, AA978395	LD28411.5prime LD Drosophila melanogaster ...	36	4.3

D15134, RICC0136A Rice cDNA, partial sequence (C0136A). 36 4.3  
 D46483, RICS11185A Rice cDNA, partial sequence (S11185\_1A). 36 4.3  
 D46618, RICS11395A Rice cDNA, partial sequence (S11395\_1A). 36 4.3  
 D46659, RICS11457A Rice cDNA, partial sequence (S11457\_1A). 36 4.3  
 D46719, RICS11572A Rice cDNA, partial sequence (S11572\_1A). 36 4.3  
 D48579, RICS14880A Rice cDNA, partial sequence (S14880\_2A). 36 4.3  
 AA802334, AA802334 GM04219.5prime GM Drosophila melanogaster ... 36 4.3  
 D46066, RICS10470A Rice cDNA, partial sequence (S10470\_1A). 36 4.3  
 D47037, RICS12104A Rice cDNA, partial sequence (S12104\_1A). 36 4.3  
 D46874, RICS11807A Rice cDNA, partial sequence (S11807\_2A). 36 4.3  
 D47174, RICS12340A Rice cDNA, partial sequence (S12340\_2A). 36 4.3  
 T04578, T04578 625 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 36 4.3  
 C83675, C83675 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3  
 D47950, RICS13762A Rice cDNA, partial sequence (S13762\_1A). 36 4.3  
 R90044, R90044 16399 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 4.3  
 D46994, RICS12013A Rice cDNA, partial sequence (S12013\_2A). 36 4.3  
 AA440820, AA440820 LD15713.5prime LD Drosophila melanogaster ... 36 4.3  
 C72089, C72089 Rice cDNA, partial sequence (E0963\_1A) 36 4.3  
 Z84004, SSZ84004 S.scrofa mRNA; expressed sequence tag (5'; ... 36 4.3  
 D47519, RICS13070A Rice cDNA, partial sequence (S13070\_1A). 36 4.3  
 C19735, C19735 Rice cDNA, partial sequence (E10858\_1A) 36 4.3  
 D47231, RICS12462A Rice cDNA, partial sequence (S12462\_1A). 36 4.3  
 D47147, RICS12293A Rice cDNA, partial sequence (S12293\_1A). 36 4.3  
 AA950198, AA950198 LD30147.5prime LD Drosophila melanogaster ... 36 4.3  
 Z47624, ATTS4480 A. thaliana transcribed sequence; clone TAI... 36 4.3  
 D45955, RICS10259A Rice cDNA, partial sequence (S10259\_1A). 36 4.3  
 D47137, RICS12280A Rice cDNA, partial sequence (S12280\_1A). 36 4.3  
 D69927, CELK093H2F C.elegans cDNA clone yk93h2 : 5' end, sin... 36 4.3  
 AA392275, AA392275 LD11117.5prime LD Drosophila melanogaster ... 36 4.3

SEQ ID NO:546

D87455, D87455 Human mRNA for KIAA0266 gene. complete cds 1164 0.0  
 Z99129, HS425C14 Human DNA sequence from clone 425C14 on chr... 42 0.20  
 D90900, D90900 Synechocystis sp. PCC6803 complete genome, 2/... 40 0.80  
 Z74281, SCYDL233W S.cerevisiae chromosome IV reading frame O... 38 3.1  
 AL021528, HS394P21 Homo sapiens DNA sequence from PAC 394P21... 38 3.1  
 Z49155, HSL83D3 Human DNA from cosmid L83d3. Huntington's Di... 38 3.1  
 U33761, HSU33761 Human cyclin A/CDK2-associated p45 (Skp2) mR... 38 3.1  
 AF052832, AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 38 3.1  
 Z98600, SPAC20G4 S.pombe chromosome I cosmid c20G4 38 3.1

Y09438, SPHUSPLUS *S.pombe hus1+* gene 38 3.1  
D29951, MUSKIF Mouse mRNA for kinesin family protein KIF1a, ... 38 3.1

## HUMAN ESTs

AA151187, AA151187 zo03c11.r1 Stratagene colon (#937204) Homo... 694 0.0  
AA824593, AA824593 oc83d10.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 670 0.0  
AA954862, AA954862 op20c03.s1 NCI\_CGAP\_Co12 Homo sapiens cDNA... 581 e-164  
T16360, T16360 NIB1193 Normalized infant brain, Bento Soares ... 517 e-145  
R54592, R54592 yg81h10.s1 Homo sapiens cDNA clone 40102 3'. 511 e-143  
AA373594, AA373594 EST85631 HSC172 cells I Homo sapiens cDNA ... 507 e-142  
AA100660, AA100660 zl90a05.r1 Stratagene colon (#937204) Homo... 383 e-104  
R42009, R42009 yg05b04.s1 Homo sapiens cDNA clone 31336 3'. 379 e-103  
AA249614, AA249614 k304l.seq.F Human fetal heart, Lambda ZAP ... 252 5e-65  
AA360633, AA360633 EST69800 T-cell lymphoma Homo sapiens cDNA... 182 4e-44  
AA053498, AA053498 zl70b11.r1 Stratagene colon (#937204) Homo... 38 1.5  
AA992442, AA992442 or85h03.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 1.5

AA065677, AA065677 mm43c03.r1 Stratagene mouse melanoma (#937... 297 4e-79  
AA529728, AA529728 vi38g12.r1 Beddington mouse embryonic regi... 42 0.035  
W91608, W91608 MTA.D10.092.A MTA adult mouse thymus library M... 42 0.035  
AA177186, AA177186 mt51a11.r1 Stratagene mouse embryonic carc... 42 0.035  
AA048008, AA048008 mj26h10.r1 Soares mouse embryo NbME13.5 14... 36 2.2  
AA637535, AA637535 vu10c02.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2  
AA726355, AA726355 vu90c09.r1 Stratagene mouse skin (#937313)... 36 2.2  
AA404025, AA404025 va31c11.r1 GuayWoodford Beier mouse kidney... 36 2.2  
AA060014, AA060014 ml34d07.r1 Stratagene mouse testis (#93730... 36 2.2  
AA870617, AA870617 vq23h10.r1 Barstead stromal cell line MPLR... 36 2.2  
AA414112, AA414112 vc64f08.s1 Knowles Solter mouse 2 cell Mus... 36 2.2  
AA764250, AA764250 vv49e09.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2

H34350, H34350 EST111226 Rat PC-12 cells, NGF-treated (9 days... 36 1.9  
C40718, C40718 *C.elegans* cDNA clone yk247f9 : 5' end. single... 36 1.9  
AA817925, AA817925 UI-R-A0-af-g-04-0-UI.s1 UI-R-A0 Rattus nor... 36 1.9  
AA955650, AA955650 UI-R-E1-fc-e-10-0-UI.s1 UI-R-E1 Rattus nor... 36 1.9

SEQ ID NO:547

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.35  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.35  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.35  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA. comple... 40 1.4  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4  
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4  
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA.... 40 1.4

## HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0  
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 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95  
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
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 AA577174, AA577174 nm86e11.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 40 0.67  
 AA215903, AA215903 hp0042.seq.F Fetal heart. Lambda ZAP Expre... 40 0.67  
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 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.6  
 H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 2.6  
 R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 2.6

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 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24  
 AA103139, AA103139 mol17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.24  
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 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.24  
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
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 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.24  
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.24  
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 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.24  
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 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.24  
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24  
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 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.24  
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 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.7  
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.7  
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.7  
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7  
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.7  
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.7  
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7  
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.7  
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.7  
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.7



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 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.7  
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.7  
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7  
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.7  
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.7  
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7  
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.7  
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.7  
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.7  
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.7  
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7  
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.7  
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7  
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.7

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 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84  
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 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84  
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 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.84  
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.84  
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.84  
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 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84  
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.84  
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.3  
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.3  
 D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.3  
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.3  
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end. singl... 36 3.3  
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 3.3  
 D46069, RICS10475A Rice cDNA, partial sequence (S10475\_1A). 36 3.3  
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 3.3  
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.3  
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.3  
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.3  
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SEQ ID NO:548

U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.34  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.34  
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 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.3  
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.3  
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.3  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.3

## HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
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 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
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 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.64  
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 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.2  
 Z33974, ATTS3035 A. thaliana transcribed sequence: clone PAP... 36 3.2  
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.2  
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.2

D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.2  
 Z32603, ATTS2731 *A. thaliana* transcribed sequence; clone PAP... 36 3.2  
 AA785775, AA785775 h4b05a1.f1 *Aspergillus nidulans* 24hr asexu... 36 3.2  
 C68472, C68472 *C.elegans* cDNA clone yk305a12 : 5' end, singl... 36 3.2  
 AA125602, AA125602 JM00M011.QM3 *Miracidia Sjc* 3/96 *Schistosom*... 36 3.2  
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.2  
 Z32602, ATTS2730 *A. thaliana* transcribed sequence; clone PAP... 36 3.2

## SEQ ID NO:549

U79271, HSU79271 Human clones 23920 and 23921 mRNA sequence 650 0.0  
 AC000395, AC000395 Genomic sequence from Human 9q34, complete... 42 0.28  
 AC004636, AC004636 *Homo sapiens* chromosome 5, P1 clone 1268h6... 42 0.28  
 M94579, HUMCEL Human carboxyl ester lipase (CEL) gene, comple... 42 0.28  
 AC002097, AC002097 *Homo sapiens* chromosome 9q34, clone 246H5,... 42 0.28  
 AB006709, AB006709 *Vibrio alginolyticus* rpoN gene for RNA po... 42 0.28  
 Z47074, CEK07C10 *Caenorhabditis elegans* cosmid K07C10, compl... 40 1.1  
 AC004755, AC004755 *Homo sapiens* chromosome 19, fosmid 37502, ... 40 1.1  
 Z28051, SCYKL051W *S.cerevisiae* chromosome XI reading frame O... 40 1.1  
 AF022655, AF022655 *Homo sapiens* cep250 centrosome associated ... 40 1.1  
 AB006708, AB006708 *Arabidopsis thaliana* genomic DNA, chromos... 40 1.1  
 AF049105, AF049105 *Homo sapiens* centrosomal Nek2-associated p... 40 1.1  
 Z28050, SCYKL050C *S.cerevisiae* chromosome XI reading frame O... 40 1.1  
 X75781, SCXI286K *S.cerevisiae* chromosome XI (28.6 kb) DNA fo... 40 1.1  
 Y16899, DMY16899 *Drosophila melanogaster* mRNA for optomotor-... 38 4.3  
 M87854, RATBARK1 *Rattus norvegicus* beta-adrenergic receptor k... 38 4.3  
 M74822, RATMHTLL Rat MHC class I TL-like protein gene, comple... 38 4.3  
 M80776, HUMBARK1A Human beta-adrenergic receptor kinase 1 mRN... 38 4.3  
 D84549, YSACA *Candida tropicalis* DNA for carnitine acetyltra... 38 4.3  
 L23127, RATRMCI *Rattus norvegicus* germline MHC class I gene, ... 38 4.3  
 AC004257, AC004257 *Homo sapiens* chromosome 19, cosmid R33209,... 38 4.3  
 U70850, CELF28F9 *Caenorhabditis elegans* cosmid F28F9 38 4.3  
 U88309, CELT23B3 *Caenorhabditis elegans* cosmid T23B3 38 4.3  
 X53421, DVCHOS18 *D. virilis* s18, s15, s19, s16 chorion prote... 38 4.3  
 D89245, D89245 *Schizosaccharomyces pombe* mRNA, partial cds, ... 38 4.3  
 AF009623, AF009623 *Parascaris univalens* PUMA1 (pumal) mRNA, c... 38 4.3  
 S48813, S48813 beta-adrenergic receptor kinase [rats, brain, ... 38 4.3  
 Z67883, CEK02A4 *Caenorhabditis elegans* cosmid K02A4, complet... 38 4.3  
 U90567, GGU90567 *Gallus gallus* glutamine rich protein mRNA, p... 38 4.3  
 M98498, BOVEZRINA *Bos taurus* ezrin mRNA, complete cds. 38 4.3  
 M34073, MUSMHT10C *Mus musculus* (clone T10-c) MHC class I cell... 38 4.3

S81843, S81843 beta-adrenergic receptor kinase 1 [Syrian hams... 38 4.3  
 X61157, HSBARK H.sapiens mRNA for beta-adrenergic receptor k... 38 4.3  
 U08438, HSNBARKS4 Human beta-adrenergic receptor kinase (ADRB... 38 4.3  
 U39674, CELC06E2 Caenorhabditis elegans cosmid C06E2. 38 4.3

## HUMAN ESTs

W29097, W29097 56d11 Human retina cDNA randomly primed sublib... 1045 0.0  
 AA886109, AA886109 ny44f05.s1 NCI\_CGAP\_Pr12 Homo sapiens cDNA... 656 0.0  
 AA829894, AA829894 oe51e12.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 650 0.0  
 AA879456, AA879456 oj91g03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 650 0.0  
 AA029201, AA029201 zk12f08.s1 Soares pregnant uterus NbHPU Ho... 650 0.0  
 AA102109, AA102109 zk87g11.s1 Soares pregnant uterus NbHPU Ho... 650 0.0  
 AA843811, AA843811 ak09c08.s1 Soares parathyroid tumor NbHPA ... 650 0.0  
 W72147, W72147 zd70f08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0  
 N51485, N51485 yz04e06.s1 Homo sapiens cDNA clone 282082 3'. 650 0.0  
 AI033069, AI033069 ow93f02.s1 Soares\_fetal\_liver\_spleen\_1NFLS... 642 0.0  
 AA161465, AA161465 zo73a06.s1 Stratagene pancreas (#937208) H... 638 0.0  
 N51277, N51277 yz14d07.s1 Homo sapiens cDNA clone 283021 3'. 636 e-180  
 N64528, N64528 yz91e06.s1 Homo sapiens cDNA clone 290434 3'. 636 e-180  
 H99906, H99906 yx32h10.s1 Homo sapiens cDNA clone 263491 3'. 636 e-180  
 AA812519, AA812519 ai79b03.s1 Soares testis NHT Homo sapiens ... 636 e-180  
 R71679, R71679 yj85e08.s1 Homo sapiens cDNA clone 155558 3'. 628 e-178  
 AA744290, AA744290 ny51d02.s1 NCI\_CGAP\_Pr18 Homo sapiens cDNA... 626 e-177  
 AI038590, AI038590 ox34e03.s1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 624 e-177  
 AA099913, AA099913 zk87g11.r1 Soares pregnant uterus NbHPU Ho... 624 e-177  
 AA083859, AA083859 zn16d06.s1 Stratagene neuroepithelium NT2R... 622 e-176  
 AA883684, AA883684 al58a05.s1 Soares NFL T GBC S1 Homo sapien... 613 e-173  
 R39448, R39448 yc95d03.s1 Homo sapiens cDNA clone 23921 3'. 593 e-167  
 R36854, R36854 yf52c07.s1 Homo sapiens cDNA clone 25899 3'. 591 e-167  
 H98684, H98684 yx17g01.s1 Homo sapiens cDNA clone 262032 3'. 585 e-165  
 R07471, R07471 ye97a06.s1 Homo sapiens cDNA clone 125650 3'. 581 e-164  
 AA910762, AA910762 ol25h06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 559 e-157  
 AA083954, AA083954 zn17d06.s1 Stratagene neuroepithelium NT2R... 555 e-156  
 AA346369, AA346369 EST52776 Fetal heart II Homo sapiens cDNA ... 545 e-153  
 R54092, R54092 yg98d07.s1 Homo sapiens cDNA clone 41818 3'. 539 e-151  
 H09074, H09074 yl97a06.s1 Homo sapiens cDNA clone 46164 3'. 535 e-150  
 N21975, N21975 yw30c10.s1 Homo sapiens cDNA clone 253746 3'. 533 e-149  
 D59844, HUM070E11A Human fetal brain cDNA 3'-end GEN-070E11. 466 e-129  
 H11525, H11525 ym15h07.s1 Homo sapiens cDNA clone 48232 3'. 442 e-122  
 AA971254, AA971254 op73c08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 442 e-122  
 W77907, W77907 zd70f08.r1 Soares fetal heart NbHH19W Homo sap... 428 e-118  
 AA878973, AA878973 oj26d11.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 389 e-106  
 AA715235, AA715235 nv10g01.s1 NCI\_CGAP\_Pi22 Homo sapiens cDNA... 357 2e-96

AA328928, AA328928 EST32475 Embryo, 12 week I Homo sapiens cD... 355 7e-96  
 AA860455, AA860455 aj80f02.s1 Soares parathyroid tumor NbHPA ... 283 2e-74  
 AA026096, AA026096 ze97a04.r1 Soares fetal heart NbHH19W Homo... 268 1e-69  
 AA026516, AA026516 ze97a04.s1 Soares fetal heart NbHH19W Homo... 172 6e-41  
 T26899, T26899 ESTDIR509 Homo sapiens cDNA clone CDDIR509 3'... 170 2e-40  
 N71178, N71178 yw30c10.r1 Homo sapiens cDNA clone 253746 5'... 165 1e-38  
 AA372290, AA372290 EST84170 Raji cells, cyclohexamide treated... 98 3e-18  
 AI038890, AI038890 ox84g12.x1 Soares\_senescent\_fibroblasts\_Nb... 40 0.53  
 D81647, HUM180D08B Human fetal brain cDNA 5'-end GEN-180D08... 38 2.1  
 AA452630, AA452630 zx33f08.r1 Soares total fetus Nb2HF8 9w Ho... 38 2.1  
 AA682624, AA682624 zi19g01.s1 Soares fetal liver spleen 1NFLS... 38 2.1  
 AA742364, AA742364 ny89c12.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.1  
 AA907234, AA907234 ol03h08.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 2.1  
 T09391, T09391 EST07284 Homo sapiens cDNA clone HIBBT71 5' en... 38 2.1  
 AA161236, AA161236 zo59h07.s1 Stratagene pancreas (#937208) H... 38 2.1  
 AA252941, AA252941 zr50g09.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1  
 AA252245, AA252245 zr64g07.s1 Soares NhHMPu S1 Homo sapiens c... 38 2.1  
 AA780678, AA780678 ac70h01.s1 Stratagene fetal retina 937202 ... 38 2.1  
 W05501, W05501 za84a12.r1 Soares fetal lung NbHL19W Homo sapi... 38 2.1  
 AI039908, AI039908 ox25f07.x1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 38 2.1  
 AA280664, AA280664 zs99f09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.1  
 AA973566, AA973566 oo46f09.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 2.1  
 N27253, N27253 yx17g01.r1 Homo sapiens cDNA clone 262032 5'... 38 2.1  
 AA995707, AA995707 os29c09.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 38 2.1  
 AI016407, AI016407 ot72e09.s1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 38 2.1  
 N70619, N70619 za84a12.s1 Homo sapiens cDNA clone 299230 3'... 38 2.1  
 AA242923, AA242923 zr64g07.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1  
 AA938631, AA938631 oo96f07.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 38 2.1  
 AA985290, AA985290 am74g03.s1 Stratagene schizo brain S11 Hom... 38 2.1

AA690806, AA690806 vt25h10.r1 Barstead mouse myotubes MPLRB5 ... 377 e-103  
 AA155014, AA155014 mr99h05.r1 Stratagene mouse embryonic carc... 180 8e-44  
 AA269966, AA269966 va57d06.r1 Soares mouse 3NME12 5 Mus muscu... 172 2e-41  
 AA089195, AA089195 mo05h11.r1 Stratagene mouse lung 937302 Mu... 163 2e-38  
 AA466212, AA466212 vg86g02.r1 Barstead mouse pooled organs MP... 68 8e-10  
 AA423476, AA423476 ve76d07.r1 Soares mouse mammary gland NbMM... 60 2e-07  
 AA597213, AA597213 vo28a05.r1 Barstead mouse irradiated colon... 40 0.19  
 AA396266, AA396266 vb45c01.r1 Soares mouse lymph node NbMLN M... 40 0.19  
 AA967806, AA967806 uh05d06.r1 Soares mouse hypothalamus NMHy ... 38 0.75  
 AA591111, AA591111 vm12c06.r1 Knowles Solter mouse blastocyst... 38 0.75  
 W65797, W65797 me14g02.r1 Soares mouse embryo NbME13.5 14.5 M... 38 0.75  
 AA153891, AA153891 mq56e05.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.75

AI019772, AI019772 ua90h02.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA472253, AA472253 vh10g05.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA230895, AA230895 mwl4g07.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.0  
 W18052, W18052 mb83g03.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.0  
 AA797681, AA797681 vx66c12.r1 Stratagene mouse skin (#937313)... 36 3.0  
 W66734, W66734 me26g05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0  
 AA968020, AA968020 uh07g01.r1 Soares mouse hypothalamus NMHy ... 36 3.0  
 AA051644, AA051644 mj55d12.r1 Soares mouse embryo NbME13.5 14... 36 3.0  
 AA162797, AA162797 mr29g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA549644, AA549644 vk80f08.s1 Knowles Solter mouse 2 cell Mus... 36 3.0  
 AA273295, AA273295 vc01e01.r1 Soares mouse lymph node NbMLN M... 36 3.0  
 AA048480, AA048480 mj33d08.r1 Soares mouse embryo NbME13.5 14... 36 3.0  
 AA098207, AA098207 mn83d01.r1 Stratagene mouse Tcell 937311 M... 36 3.0  
 AA027381, AA027381 mi05c06.r1 Soares mouse placenta 4NbMP13.5... 36 3.0  
 AA544474, AA544474 vk33h06.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA416466, AA416466 vd15c09.s1 Knowles Solter mouse 2 cell Mus... 36 3.0  
 AA285999, AA285999 vb88h08.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA175025, AA175025 ms85f06.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA544386, AA544386 vk33f06.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA175557, AA175557 ms96g04.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA711924, AA711924 vu59f09.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA734052, AA734052 vv22c10.r1 Stratagene mouse heart (#937316... 36 3.0  
 W53738, W53738 md12a12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0  
 AA611837, AA611837 vo82a06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.0  
 AA879531, AA879531 vv96f06.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA288625, AA288625 vb23g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
  
 AA784124, AA784124 d2b06a1.fl Aspergillus nidulans 24hr asexu... 38 0.67  
 AI044911, AI044911 UI-R-C1-kk-e-05-0-UI.s1 UI-R-C1 Rattus nor... 36 2.6  
 AA550452, AA550452 1605m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 2.6  
 F20017, ATTS6056 A. thaliana transcribed sequence; clone TAP... 36 2.6  
 AA786697, AA786697 k5d01a1.fl Aspergillus nidulans 24hr asexu... 36 2.6  
 AA433457, AA433457 SW3ICA2345SK Brugia malayi infective larva... 36 2.6

SEQ ID NO:550

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.20  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.20  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.20  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 0.80

AC004301, AC004301 *Drosophila melanogaster* DNA sequence (P1 D... 40 0.80  
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 40 0.80  
 Y14330, HSY14330 *Homo sapiens* partial mRNA for jagged2 protein 38 3.2  
 AF003521, AF003521 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2  
 AF029778, AF029778 *Homo sapiens* Jagged2 (JAG2) mRNA, complete... 38 3.2  
 AF020201, AF020201 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2  
 Z71523, SCYNL247W *S.cerevisiae* chromosome XIV reading frame ... 38 3.2  
 AF029779, AF029779 *Homo sapiens* hJAG2.del-E6 (JAG2) mRNA, alt... 38 3.2  
 U70049, RNU70049 *Rattus norvegicus* jagged2 precursor gene, pa... 38 3.2  
 X96722, SCCHXIVL *S.cerevisiae* DNA region from chromosome XIV... 38 3.2  
 AF005938, AF005938 *Cavia porcellus* L-type voltage-dependent c... 38 3.2  
 X78972, SBSTRBF *S.bluensis* ISP 5564 genes strB and strF 38 3.2  
 X94912, HSPR22 *H.sapiens* Pr22 gene 38 3.2

# HUMAN ESTs

AA860926, AA860926 ak22d06.s1 Soares testis NHT *Homo sapiens* ... 650 0.0  
 AA348243, AA348243 EST54707 Hippocampus I *Homo sapiens* cDNA 5... 513 e-144  
 AA551799, AA551799 nk04a11.s1 NCI\_CGAP\_Co2 *Homo sapiens* cDNA ... 363 2e-98  
 AA327309, AA327309 EST30621 Colon I *Homo sapiens* cDNA 5' end 353 2e-95  
 AA344913, AA344913 EST50856 Gall bladder II *Homo sapiens* cDNA... 337 1e-90  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) *Homo*... 317 1e-84  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) *Homo*... 317 1e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR *Homo sapie*... 42 0.098  
 AI005204, AI005204 ou60c12.x1 NCI\_CGAP\_Br2 *Homo sapiens* cDNA ... 40 0.39  
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39  
 AI005324, AI005324 ou13h07.x1 Soares\_NFL\_T\_GBC\_S1 *Homo sapien*... 40 0.39  
 AA416559, AA416559 zul8c03.r1 Soares NhHMPu S1 *Homo sapiens* c... 40 0.39  
 AA262162, AA262162 zs25b12.r1 NCI\_CGAP\_GCB1 *Homo sapiens* cDNA... 40 0.39  
 AA824270, AA824270 aj29f01.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA826741, AA826741 85f12.s1 NCI\_CGAP\_Pr24 *Homo sapiens* cDNA... 40 0.39  
 AA813115, AA813115 aj44d06.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39  
 AA804907, AA804907 oa89a01.s1 NCI\_CGAP\_GCB1 *Homo sapiens* cDNA... 40 0.39  
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA618498, AA618498 np30a11.s1 NCI\_CGAP\_Pr22 *Homo sapiens* cDNA... 40 0.39  
 AA503727, AA503727 ne49g02.s1 NCI\_CGAP\_Co3 *Homo sapiens* cDNA ... 40 0.39  
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39  
 AA759377, AA759377 ah54a10.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA629243, AA629243 zu77e03.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA903406, AA903406 ok62c11.s1 NCI\_CGAP\_GCB4 *Homo sapiens* cDNA ... 40 0.39  
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.39



AA160827, AA160827 zo62e01.sl Stratagene pancreas (#937208) H... 40 0.39  
 AA577174, AA577174 nm86e11.sl NCI\_CGAP\_Co9 Homo sapiens cDNA ... 40 0.39  
 AA969632, AA969632 op38h05.sl Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.39  
 N72025, N72025 yz96g02.sl Homo sapiens cDNA clone 290930 3'. 40 0.39  
 AA974988, AA974988 on59b06.sl Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.39  
 W32428, W32428 zc05c12.sl Soares parathyroid tumor NbHPA Homo... 40 0.39  
 N21678, N21678 yx63g01.sl Soares melanocyte 2NbHM Homo sapien... 40 0.39  
 AA860208, AA860208 ak48c10.sl Soares testis NHT Homo sapiens ... 40 0.39  
 AA814296, AA814296 nz07d08.sl NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.39  
 AA806381, AA806381 oc22g05.sl NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.39  
 AA435587, AA435587 zt85d07.sl Soares testis NHT Homo sapiens ... 40 0.39  
 W45005, W45005 zc05c12.rl Soares parathyroid tumor NbHPA Homo... 40 0.39  
 AA393904, AA393904 zt85e06.rl Soares testis NHT Homo sapiens ... 40 0.39  
 AA759038, AA759038 ah75h11.sl Soares testis NHT Homo sapiens ... 40 0.39  
 AA927863, AA927863 om18a08.sl Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.39  
 AA461270, AA461270 zx63b07.rl Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA417295, AA417295 zu18c03.sl Soares NhHMPu S1 Homo sapiens c... 40 0.39  
 W47466, W47466 zc34h02.rl Soares senescent fibroblasts NbHSF ... 40 0.39  
 AA262229, AA262229 zs25b12.sl NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.39  
 AA587486, AA587486 nn84e09.sl NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.39  
 AA401079, AA401079 zv66d01.sl Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA872272, AA872272 oh72a11.sl NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.39  
 W47341, W47341 zc34h02.sl Soares senescent fibroblasts NbHSF ... 40 0.39  
 N72024, N72024 yz96g01.sl Homo sapiens cDNA clone 290928 3'. 40 0.39  
 N35076, N35076 yy19b08.sl Homo sapiens cDNA clone 271671 3'. 40 0.39  
 AI040354, AI040354 oy33d12.x1 Soares\_parathyroid\_tumor\_NbHPA ... 40 0.39  
 AA946650, AA946650 oq38h09.sl NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.39  
 AA022495, AA022495 ze70e04.sl Soares fetal heart NbHH19W Homo... 40 0.39  
 AA873216, AA873216 oh70f04.sl NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.39  
 R82551, R82551 yj19d06.rl Homo sapiens cDNA clone 149195 5'. 38 1.5  
 H30248, H30248 yp42a01.sl Homo sapiens cDNA clone 190056 3'. 38 1.5  
 AA161105, AA161105 zo58c05.sl Stratagene pancreas (#937208) H... 38 1.5  
 AA948291, AA948291 oq34d02.sl NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 1.5  
 AA416734, AA416734 zu08c01.sl Soares testis NHT Homo sapiens ... 38 1.5  
 AA431486, AA431486 zw72g01.sl Soares testis NHT Homo sapiens ... 38 1.5  
 AA416815, AA416815 zu08c01.rl Soares testis NHT Homo sapiens ... 38 1.5

AA616807, AA616807 vn68c05.rl Barstead mouse irradiated colon... 180 6e-44  
 AA467482, AA467482 ve01a10.rl Soares mouse NbMH Mus musculus ... 40 0.14  
 AA543280, AA543280 vj80h05.rl Soares mouse mammary gland NbMM... 40 0.14  
 AA009071, AA009071 mg87b11.rl Soares mouse embryo NbME13.5 14... 40 0.14  
 AA106439, AA106439 ml59a08.rl Stratagene mouse testis (#93730... 40 0.14

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 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.14  
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.14  
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.14  
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.14  
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 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.14  
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.14  
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14  
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
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 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.14  
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.14  
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14  
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.14  
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.14  
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.55  
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2  
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 2.2  
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 2.2  
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 2.2  
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 2.2  
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 2.2  
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2  
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2  
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 2.2  
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 2.2  
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.2  
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 2.2  
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 2.2  
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 2.2  
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 2.2  
 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 2.2  
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 2.2

AA856298, AA856298 vw99b01.rl Soares 2NbMT Mus musculus cDNA ... 36 2.2  
 AA966976, AA966976 ua38f11.rl Soares mouse mammary gland NbMM... 36 2.2

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.031  
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 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.48  
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48  
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48  
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48  
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48  
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.48  
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.48  
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.48  
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.48  
 AA859542, AA859542 UI-R-E0-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48  
 H32878, H32878 EST108396 Rat FC-12 cells, untreated Rattus sp... 36 1.9  
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 1.9  
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 1.9  
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 1.9  
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 1.9  
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 1.9  
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 1.9  
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 1.9  
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 1.9

SEQ ID NO:551

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.36  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.36  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.36  
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA... 40 1.4  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4  
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4

#### HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

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 AA551799, AA551799 nk04a11.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 363 4e-98  
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95  
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17  
 AA877455, AA877455 ob33g01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.68  
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.68  
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.68  
 AA573297, AA573297 nk98d09.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.68  
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.68  
 AA514777, AA514777 ni24b01.s1 NCI\_CGAP\_Co4 Homo sapiens cDNA ... 40 0.68  
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.68  
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.68  
 AA888147, AA888147 04h11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.68  
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.68  
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 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.7  
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.7  
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 AA948291, AA948291 oq34d02.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 2.7  
 R14449, R14449 yf81h09.r1 Homo sapiens cDNA clone 29034 5'. 38 2.7  
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 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24  
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24  
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24  
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24  
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 AA250010, AA250010 mz59b12.r1 Soares mouse lymph node NbMLN M... 38 0.97  
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.97  
 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 0.97  
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 3.8  
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.8  
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 3.8  
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.8  
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 3.8  
 AA103139, AA103139 mol7f05.r1 Life Tech mouse embryo 13 5dpc ... 36 3.8

AA840087, AA840087 uc99h12.rl Soares mouse uterus NMPu Mus mu... 36 3.8  
 AA543280, AA543280 vj80h05.rl Soares mouse mammary gland NbMM... 36 3.8  
 AA007762, AA007762 mg76b03.rl Soares mouse embryo NbME13.5 14... 36 3.8  
 AA014223, AA014223 mh20a03.rl Soares mouse placenta 4NbMP13.5... 36 3.8  
 AA591243, AA591243 vm18c04.rl Knowles Solter mouse blastocyst... 36 3.8  
 AA921560, AA921560 vy52c06.rl Stratagene mouse lung 937302 Mu... 36 3.8  
 W20935, W20935 mb96c07.rl Soares mouse p3NMF19.5 Mus musculus... 36 3.8  
 AA793845, AA793845 vr35e12.rl Barstead mouse myotubes MPLRB5 ... 36 3.8  
 AA856298, AA856298 vw99b01.rl Soares 2NbMT Mus musculus cDNA ... 36 3.8  
 AA833479, AA833479 uc91c03.rl Soares mouse uterus NMPu Mus mu... 36 3.8  
 AA218431, AA218431 my07e05.rl Barstead mouse lung MPLRB2 Mus ... 36 3.8  
 AA089210, AA089210 mo05d10.rl Stratagene mouse lung 937302 Mu... 36 3.8  
 AI047609, AI047609 uh63g07.rl Soares mouse embryonic stem cel... 36 3.8  
 AA797372, AA797372 vw27b08.rl Soares mouse mammary gland NbMM... 36 3.8  
 AA138067, AA138067 mq37c11.rl Barstead MPLRB1 Mus musculus cD... 36 3.8  
 W83172, W83172 mf09a06.rl Soares mouse p3NMF19.5 Mus musculus... 36 3.8  
 AA542324, AA542324 vk53e07.rl Stratagene mouse Tcell 937311 M... 36 3.8  
 AA967316, AA967316 vj47a03.rl Stratagene mouse skin (#937313)... 36 3.8  
 AI035925, AI035925 ub49e05.rl Soares mouse mammary gland NbMM... 36 3.8  
 AA497479, AA497479 vh29b12.rl Soares mouse mammary gland NbMM... 36 3.8  
 W87202, W87202 mf55g08.rl Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
 AA016868, AA016868 mh36e12.rl Soares mouse placenta 4NbMP13.5... 36 3.8  
 AA467482, AA467482 ve01a10.rl Soares mouse NbMH Mus musculus ... 36 3.8  
 AA014768, AA014768 mi66h04.rl Soares mouse embryo NbME13.5 14... 36 3.8  
 AA711859, AA711859 vu59c10.rl Soares mouse mammary gland NbMM... 36 3.8  
 AA530735, AA530735 vj32g11.rl Stratagene mouse diaphragm (#93... 36 3.8  
 AA009071, AA009071 mg87b11.rl Soares mouse embryo NbME13.5 14... 36 3.8  
 AA711873, AA711873 vu28e06.rl Barstead mouse myotubes MPLRB5 ... 36 3.8  
 AA645119, AA645119 vs72d03.rl Stratagene mouse skin (#937313)... 36 3.8  
 AA106301, AA106301 ml81a09.rl Stratagene mouse kidney (#93731... 36 3.8  
 AA111190, AA111190 mp66b11.rl Soares 2NbMT Mus musculus cDNA ... 36 3.8  
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.8  
 AA796056, AA796056 vo65d01.rl Soares mouse mammary gland NbMM... 36 3.8  
 AA230661, AA230661 mw15f08.rl Soares mouse 3NME12 5 Mus muscu... 36 3.8  
 AA033481, AA033481 mi42b07.rl Soares mouse embryo NbME13.5 14... 36 3.8  
 AA000268, AA000268 mg32e09.rl Soares mouse embryo NbME13.5 14... 36 3.8  
 AI048515, AI048515 uh61e08.rl Soares mouse embryonic stem cel... 36 3.8  
 W61547, W61547 md57a02.rl Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
 AA790448, AA790448 vw04f09.rl Soares mouse mammary gland NbMM... 36 3.8  
 AA824205, AA824205 vy20g08.rl Stratagene mouse macrophage (#9... 36 3.8  
 AA475425, AA475425 vh20g09.rl Soares mouse mammary gland NbMM... 36 3.8  
 W62989, W62989 md88h12.rl Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
 W77724, W77724 me84h06.rl Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
 AA239210, AA239210 mx89e02.rl Soares mouse NML Mus musculus c... 36 3.8

276X

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.055  
 AA891284, AA891284 EST195087 Normalized rat heart, Bento Soar... 40 0.22  
 Z83055, RNZ83055 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22  
 AI010967, AI010967 EST205418 Normalized rat muscle, Bento Soa... 40 0.22  
 AA852049, AA852049 EST194818 Normalized rat spleen, Bento Soa... 40 0.22  
 H33489, H33489 EST109542 Rat PC-12 cells, NGF-treated (9 days... 40 0.22  
 AA799616, AA799616 EST189113 Normalized rat heart, Bento Soar... 40 0.22  
 Z83044, RNZ83044 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22  
 AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.86  
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.86  
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.86  
 AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.4  
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.4  
 AA943364, AA943364 EST198863 Normalized rat brain. Bento Soar... 36 3.4  
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.4  
 AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.4  
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.4  
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.4  
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.4  
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.4  
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.4  
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.4  
 D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.4  
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.4  
 AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.4  
 D46069, RICS10475A Rice cDNA, partial sequence (S10475\_1A). 36 3.4

SEQ ID NO:552

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.38  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.38  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.38  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.5  
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.5  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.5

## HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143  
 AA551799, AA551799 nk04a11.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 363 4e-98  
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95  
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.18  
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.72  
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.72  
 AA877455, AA877455 ob33g01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.72  
 AA573297, AA573297 nk98d09.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.72  
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.72  
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.72  
 AA514777, AA514777 ni24b01.s1 NCI\_CGAP\_Co4 Homo sapiens cDNA ... 40 0.72  
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.72  
 AA888147, AA888147 04h11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.72  
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.72  
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.8  
 N25839, N25839 yx22e05.r1 Homo sapiens cDNA clone 262496 5'. 38 2.8  
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.8  
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.8  
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.8  
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.8  
 AA948291, AA948291 oq34d02.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 2.8

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43  
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.26  
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.26  
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.26  
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.26  
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.26  
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.26  
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 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 1.0  
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 1.0  
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 4.0  
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 4.0  
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.0  
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.0  
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 4.0  
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 4.0

AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 4.0  
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 4.0  
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 4.0  
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 4.0  
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 4.0  
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 36 4.0  
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 4.0  
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 4.0  
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 4.0  
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 4.0  
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 4.0  
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0  
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 4.0  
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 4.0  
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 4.0  
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 4.0  
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0  
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 4.0  
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 4.0  
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA230661, AA230661 mwl5f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.0  
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 4.0  
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0  
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 4.0  
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0  
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 4.0  
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 36 4.0  
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0  
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0  
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.0  
 AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 4.0  
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 4.0  
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 4.0  
 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 4.0  
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 4.0



AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.058  
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.90  
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.90  
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.90  
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.6  
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.6  
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.6  
AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 3.6  
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.6  
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.6  
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.6  
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.6  
D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.6  
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.6  
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.6  
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.6  
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.6  
D46069, RICS10475A Rice cDNA, partial sequence (S10475\_1A). 36 3.6  
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.6

SEQ ID NO:553

Z99297, HS262D12 Homo sapiens DNA sequence from PAC 262D12 o... 1963 0.0  
Z81540, CEF46B3 Caenorhabditis elegans cosmid F46B3, complet... 40 0.89  
U67488, U67488 Methanococcus jannaschii section 30 of 150 of ... 38 3.5  
AE000786, AE000786 Borrelia burgdorferi plasmid lp28-2, compl... 38 3.5  
L02053, OMMGSHTR1 Ommastrephes sloani glutathione transferase... 38 3.5  
AC004521, ATAC004521 Arabidopsis thaliana chromosome II BAC F... 38 3.5  
L41250, DROGPDHN Drosophila nebulosa glycerol-3-phosphate deh... 38 3.5  
AE000619, HPAE000619 Helicobacter pylori section 97 of 134 of... 38 3.5  
U39720, Mycoplasma genitalium ackA, licA, mucB, rpL10, rpL32... 38 3.5  
AC004533, HUAC004533 Homo sapiens Chromosome 16 BAC clone CIT... 38 3.5  
U62292, HSU62292 Human elastin (ELN) gene, partial cds 38 3.5

#### HUMAN ESTs

W02630, W02630 za52c02.rl Soares fetal liver spleen INFLS Hom... 1009 0.0  
AA557183, AA557183 nl74f12.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 874 0.0  
AA761171, AA761171 nz09e11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 866 0.0  
AA976975, AA976975 oq26g11.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 854 0.0  
AA449515, AA449515 zx06b11.rl Soares total fetus Nb2HF8 9w Ho... 848 0.0

AA678392, AA678392 zi26h10.s1 Soares fetal liver spleen 1NFLS... 848 0.0  
AA909198, AA909198 ol12d06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 831 0.0  
W79208, W79208 zd79g05.r1 Soares fetal heart NbHH19W Homo sap... 813 0.0  
W03125, W03125 za53c02.r1 Soares fetal liver spleen 1NFLS Hom... 807 0.0  
W94750, W94750 ze13h08.r1 Soares fetal heart NbHH19W Homo sap... 785 0.0  
AA354894, AA354894 EST63217 Jurkat T-cells V Homo sapiens cDN... 771 0.0  
H70075, H70075 yr92b03.r1 Homo sapiens cDNA clone 212717 5'. 745 0.0  
W77859, W77859 zd70b08.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0  
AA425424, AA425424 zw48f03.s1 Soares total fetus Nb2HF8 9w Ho... 718 0.0  
AA476893, AA476893 zu29f09.r1 Soares ovary tumor NbHOT Homo s... 688 0.0  
AA456676, AA456676 aa01h02.s1 Soares NhHMPu S1 Homo sapiens c... 688 0.0  
AA662309, AA662309 nu97c11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 668 0.0  
W72135, W72135 zd70b08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0  
N74362, N74362 za52c02.s1 Homo sapiens cDNA clone 296162 3'. 622 e-176  
N66917, N66917 za47d09.s1 Homo sapiens cDNA clone 295697 3'. 585 e-165  
AA251287, AA251287 zs04c06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 583 e-164  
AA971082, AA971082 op70h01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 567 e-160  
W78165, W78165 zd79g05.s1 Soares fetal heart NbHH19W Homo sap... 565 e-159  
AA253290, AA253290 zr71g03.r1 Soares NhHMPu S1 Homo sapiens c... 559 e-157  
AA729063, AA729063 nw22f08.s1 NCI\_CGAP\_GCB0 Homo sapiens cDNA... 557 e-157  
AA987313, AA987313 or81h06.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 553 e-155  
AA300954, AA300954 EST13832 Testis tumor Homo sapiens cDNA 5'... 541 e-152  
AA425594, AA425594 zw48f03.r1 Soares total fetus Nb2HF8 9w Ho... 529 e-148  
N24014, N24014 yx87g10.s1 Homo sapiens cDNA clone 268770 3'. 523 e-146  
AA947355, AA947355 od86e12.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA ... 504 e-140  
AA121074, AA121074 zl88b06.s1 Stratagene colon (#937204) Homo... 460 e-127  
AA742964, AA742964 ny15d01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 454 e-126  
AA306814, AA306814 EST177885 Colon carcinoma (HCC) cell line ... 452 e-125  
W87699, W87699 zh65b11.r1 Soares fetal liver spleen 1NFLS S1 ... 446 e-123  
W87700, W87700 zh65b11.s1 Soares fetal liver spleen 1NFLS S1 ... 438 e-121  
AA449084, AA449084 zx06b11.s1 Soares total fetus Nb2HF8 9w Ho... 398 e-109  
N99231, N99231 zb76f11.s1 Soares senescent fibroblasts NbHSF ... 391 e-106  
N49900, N49900 yv24d04.s1 Homo sapiens cDNA clone 243655 3'. 383 e-104  
AA782911, AA782911 ai62a10.s1 Soares testis NHT Homo sapiens ... 365 6e-99  
AA936553, AA936553 on23g11.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 361 9e-98  
N74414, N74414 za53c02.s1 Homo sapiens cDNA clone 296258 3'. 353 2e-95  
AA834628, AA834628 od98a10.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA ... 341 8e-92  
AA693756, AA693756 zi55f11.s1 Soares fetal liver spleen 1NFLS... 341 8e-92  
AA909616, AA909616 ol09d06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 341 8e-92  
H69662, H69662 yr92b03.s1 Homo sapiens cDNA clone 212717 3'. 321 8e-86  
AA249558, AA249558 jj7521.seq.F Human fetal heart, Lambda ZAP... 317 1e-84  
AA911960, AA911960 oh88g08.s1 NCI\_CGAP\_Co8 Homo sapiens cDNA ... 317 1e-84  
AA969099, AA969099 op55e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 303 2e-80  
AA766191, AA766191 oa12g08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 212 5e-53  
AA689312, AA689312 nx05e10.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 200 2e-49

AA418586, AA418586 zv93e05.r1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44  
 AA418570, AA418570 zv93e05.s1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44  
 AA534939, AA534939 nf82f03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 167 3e-39  
 AA888430, AA888430 nw74e05.s1 NCI\_CGAP\_Pr12 Homo sapiens cDNA... 167 3e-39  
 N50003, N50003 yv24d04.r1 Homo sapiens cDNA clone 243655 5' s... 149 6e-34  
 AA535102, AA535102 nf84f06.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 135 1e-29  
 AA262335, AA262335 zr71g03.s1 Soares NhHMPu S1 Homo sapiens c... 129 6e-28  
 AA766681, AA766681 oa34c05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 105 9e-21  
 AA761492, AA761492 nz27a05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 101 1e-19  
 AA688350, AA688350 nv15a05.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 90 5e-16  
 AA347041, AA347041 EST53285 Fetal heart II Homo sapiens cDNA ... 76 8e-12  
 T94395, T94395 ye35e02.s1 Homo sapiens cDNA clone 119738 3'. 46 0.007  
 AA833565, AA833565 aj46a02.s1 Soares testis NHT Homo sapiens ... 46 0.007  
 AA095460, AA095460 l4630.seq.F Fetal heart, Lambda ZAP Expres... 40 0.43  
 AA904415, AA904415 ok07e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.43  
 AI018800, AI018800 ov32h04.x1 Soares\_testis\_NHT Homo sapiens ... 38 1.7  
 AA631083, AA631083 nq77e07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 1.7

AA399772, AA399772 vd70g05.r1 Beddington mouse embryonic regi... 347 5e-94  
 AA467106, AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 309 1e-82  
 AI046844, AI046844 uh55c11.r1 Soares mouse embryonic stem cel... 208 3e-52  
 AA475075, AA475075 vh11g05.r1 Soares mouse mammary gland NbMM... 194 4e-48  
 AA646094, AA646094 vs31e06.r1 Stratagene mouse Tcell 937311 M... 186 1e-45  
 AA390020, AA390020 vb30e07.r1 Soares mouse lymph node NbMLN M... 170 6e-41  
 AA245553, AA245553 my52g04.r1 Barstead mouse pooled organs MP... 170 6e-41  
 AA930741, AA930741 vs57b02.r1 Stratagene mouse skin (#937313)... 155 4e-36  
 W62610, W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 117 8e-25  
 AA239270, AA239270 my40e01.r1 Barstead mouse pooled organs MP... 109 2e-22  
 AA015148, AA015148 mh16e01.r1 Soares mouse placenta 4NbMP13.5... 54 1e-05  
 AA764095, AA764095 vw09h02.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.61  
 AA238570, AA238570 my35h02.r1 Barstead mouse pooled organs MP... 38 0.61  
 AA600576, AA600576 vm75f08.r1 Knowles Solter mouse blastocyst... 38 0.61  
 AA636273, AA636273 vq76a10.s1 Knowles Solter mouse 2 cell Mus... 36 2.4  
 AA051407, AA051407 mj41f08.r1 Soares mouse embryo NbME13.5 14... 36 2.4  
 AA823136, AA823136 vw41b03.r1 Soares mouse mammary gland NbMM... 36 2.4  
 W83831, W83831 mf26a06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4  
 D77944, MUSC0D06 Mouse embryonal carcinoma F9 cell cDNA, C0D06 36 2.4  
 AA915408, AA915408 vz29h04.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.4  
 AI047229, AI047229 uh63a09.r1 Soares mouse embryonic stem cel... 36 2.4  
 AA271880, AA271880 va73d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4  
 AA475165, AA475165 vg95f01.r1 Barstead mouse pooled organs MP... 36 2.4  
 AA619774, AA619774 vl58a05.s1 Knowles Solter mouse 2 cell Mus... 36 2.4

AA673116, AA673116 vn49g11.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4  
 AA870623, AA870623 vq24a07.r1 Barstead stromal cell line MPLR... 36 2.4  
 W58907, W58907 md52f12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4  
 AA690593, AA690593 vu53d05.r1 Soares mouse mammary gland NbMM... 36 2.4  
 AA754801, AA754801 vu21f03.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4  
 AA271607, AA271607 va72a12.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4  
 AA064256, AA064256 mj66a03.r1 Soares mouse p3NMF19.5 Mus musc... 36 2.4  
 AA475144, AA475144 vg95d01.r1 Barstead mouse pooled organs MP... 36 2.4  
 AA197736, AA197736 mv02g08.r1 GuayWoodford Beier mouse kidney... 36 2.4

AA817944, AA817944 UI-R-A0-ag-e-01-0-UI.s1 UI-R-A0 Rattus nor... 40 0.14  
 F14714, SSC8B01 S.scrofa mRNA; expressed sequence tag (5'; c... 38 0.54  
 H91505, H91505 SWMFA089SK Brugia malayi microfilaria cDNA (S... 36 2.1  
 AA998610, AA998610 UI-R-C0-if-c-04-0-UI.s1 UI-R-C0 Rattus nor... 36 2.1  
 AA893562, AA893562 EST197365 Normalized rat liver, Bento Soar... 36 2.1  
 AI008397, AI008397 EST202848 Normalized rat embryo. Bento Soa... 36 2.1

SEQ ID NO:554

Z92544, HS313D11 Human DNA sequence from cosmid 313D11 from ... 700 0.0  
 Z46940, HSPRMTNP2 H.sapiens PRM1 gene. PRM2 gene and TNP2 gene 44 0.048  
 U85039, TMU85039 Theileria mutans 32 kDa immunodominant pirop... 42 0.19  
 U85251, TMU85251 Theileria mutans 32 kDa immunodominant pirop... 42 0.19  
 AF003630, AF003630 Theileria mutans clone 15, 32 kDa immunodo... 42 0.19  
 AF003629, AF003629 Theileria mutans clone 9, 32 kDa immunodom... 42 0.19  
 AB007884, AB007884 Homo sapiens KIAA0424 mRNA, partial cds 42 0.19  
 U85040, TMU85040 Theileria mutans 32 kDa immunodominant pirop... 42 0.19  
 Z97343, ATFCA8 Arabidopsis thaliana DNA chromosome 4, ESSA I... 40 0.75  
 L19655, TOSRNA1X Tomato ringspot virus polyprotein (RNA-1) ge... 40 0.75  
 M73822, TOSRNA1A Tomato ringspot virus RNA1 gene, 5' end. 40 0.75  
 L02543, BOVMTNNT Bos taurus nicotinamide nucleotide transhydr... 40 0.75  
 J03534, BOVNAD Bovine mitochondrial nicotinamide nucleotide t... 40 0.75  
 M62862, TRBRTE Trypanosoma cruzi retrotransposon encoding gag... 40 0.75  
 X72711, MMREPCFC M.musculus mRNA for replication factor C, l... 38 3.0  
 M88489, MUSNBP Mus musculus nonamer binding protein mRNA, com... 38 3.0  
 U36441, MMU36441 Mus musculus differentiation specific elemen... 38 3.0  
 AB002354, AB002354 Human mRNA for KIAA0356 gene, complete cds 38 3.0  
 J03149, CATFMSC Cat (F.domesticus) c-fms proto-oncogene mRNA ... 38 3.0  
 J05475, CHKVICOLL Chicken type VI collagen alpha 2 (VI) subun... 38 3.0

AF038163, AF038163 Homo sapiens interleukin-15 (IL-15) gene, ... 38 3.0  
 X75917, HSFBMBF H.sapiens mRNA for fetal beta-MHC binding fa... 38 3.0  
 X06542, DMHSPG3 Drosophila heat shock gene 3 from 67B locus 38 3.0  
 D17315, DRODAGK Fruit fly mRNA for diacylglycerol kinase, co... 38 3.0  
 Z58600, HS45E3F H.sapiens CpG DNA, clone 45e3, forward read ... 38 3.0  
 D78638, D78638 Xenopus laevis mRNA for DNA (cytosine-5-)-met... 38 3.0  
 Z49204, MMNADPTRH M.musculus mRNA for NADP transhydrogenase. 38 3.0  
 L10425, BPEMETC Bordetella avium beta-cystathionase-lyase (me... 38 3.0  
 U01222, U01222 Mus musculus activator 1 large subunit (A1-p14... 38 3.0  
 U15037, MMU15037 Mus musculus replication factor C large subu... 38 3.0  
 K01643, FCSSMONC Feline sarcoma virus (McDonough strain) tran... 38 3.0  
 Z57538, HS183C6F H.sapiens CpG DNA, clone 183c6, forward rea... 38 3.0  
 U07157, MMU07157 Mus musculus ISRE-binding protein (IBF-1) mR... 38 3.0  
 Z64961, HS183F7R H.sapiens CpG DNA, clone 183f7, reverse rea... 38 3.0

#### HUMAN ESTs

#### SEQ ID NO:555

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 916 0.0  
 S51239, S51239 calreticulin [Aplysia californica=marine snail... 48 0.005  
 Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.019  
 AF022814, AF022814 Fugu rubripes transcription factor (SLP-1)... 44 0.073  
 X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.29  
 U63063, SCU63063 Saccharomyces cerevisiae something about sil... 42 0.29  
 X63501, SCRPC53 S.cerevisiae RPC53 gene for RNA polymerase C... 42 0.29  
 U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.29  
 Z74201, SCYDL153C S.cerevisiae chromosome IV reading frame O... 42 0.29  
 U66032, MTU66032 Methanosarcina thermophila CO dehydrogenase/... 42 0.29  
 Z95620, SPBC3D6 S.pombe chromosome II cosmid c3D6 42 0.29  
 X97751, SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RP... 42 0.29  
 X65541, ATCAN A.thaliana mRNA for carbonic anhydrase 42 0.29  
 L14750, ATHCARANHY Arabidopsis thaliana carbonic anhydrase ge... 42 0.29  
 U00995, U00995 Rattus norvegicus TA1 mRNA. complete cds. 40 1.1  
 S73876, S73876 FPR3=FKBP-70 [Saccharomyces cerevisiae, Genomi... 40 1.1  
 U12825, SCU12825 Saccharomyces cerevisiae transcription facto... 40 1.1  
 Z74237, SCYDL189W S.cerevisiae chromosome IV reading frame O... 40 1.1  
 U76906, REU76906 Rhizobium etli FixK (fixK). FixN (fixN). mon... 40 1.1

- AF050157, MMHC135G15 *Mus musculus* major histocompatibility lo... 40 1.1
- X58857, SCPPH22 *S.cerevisiae* PPH22 gene for protein phosphat... 40 1.1
- X79379, SCPROIS. *S.cerevisiae* gene for proline isomerase 40 1.1
- Z68341, CEF01G4 *Caenorhabditis elegans* cosmid F01G4, complet... 40 1.1
- M17192, MUSHOX1 Mouse homeodomain protein (Hox1.1) mRNA, comp... 40 1.1
- U50307, CELF43H9 *Caenorhabditis elegans* cosmid F43H9. 40 1.1
- S73144, S73144 bone sialoprotein [cattle, fetal bone cells, m... 40 1.1
- L34569, YSCFPR3A *Saccharomyces cerevisiae* (clone pBYNG1) prol... 40 1.1
- D78303, D78303 *Rattus norvegicus* YT521 mRNA for RNA splicing... 40 1.1
- X83276, SCDNAIV *S.cerevisiae* DNA for ORFs from chromosome IV 40 1.1
- U54558, HSU54558 Human translation initiation factor eIF3 p66... 40 1.1
- Z50109, CEC09H10 *Caenorhabditis elegans* cosmid C09H10, compl... 40 1.1
- X56983, EAVATP1 *E.arvense* gene for catalytic 70kDa V-ATPase ... 40 1.1
- AB011125, AB011125 *Homo sapiens* mRNA for KIAA0553 protein, p... 40 1.1
- Z46373, SC8248 *S.cerevisiae* chromosome XIII cosmid 8248 40 1.1
- AF039042, CELZK697 *Caenorhabditis elegans* cosmid ZK697 40 1.1
- Z28028, SCYKL028W *S.cerevisiae* chromosome XI reading frame O... 40 1.1
- AC005266, AC005266 *Homo sapiens* chromosome 19, cosmid F23465,... 38 4.5
- U60822, HSU60822 Human dystrophin (DMD) gene, exons 7, 8 and ... 38 4.5
- AJ003141, HVAJ3141 *Hordeum vulgare* mRNA for stress-related p... 38 4.5
- M26250, CRAGAP43 Goldfish (*C.auratus*) growth-associated prote... 38 4.5
- X95267, GGRRYR3 *G.gallus* mRNA for ryanodine receptor type 3 38 4.5
- L37092, MUSCDPK *Mus musculus* cyclin-dependent kinase homologu... 38 4.5
- Z72507, CEF17C11 *Caenorhabditis elegans* cosmid F17C11, compl... 38 4.5
- U29608, DMU29608 *Drosophila melanogaster* large tumor suppress... 38 4.5
- Z49072, CET24A11 *Caenorhabditis elegans* cosmid T24A11, compl... 38 4.5
- M83142, RATBGASTR *Rattus norvegicus* beta-galactoside-alpha 2,... 38 4.5
- Z20656, HSCAMHCA *Homo sapiens* of cardiac alpha-myosin heavy ... 38 4.5
- M82937, YSACS2A *Candida albicans* chitin synthase 2 (CHS2) gen... 38 4.5
- U28888, MMU28888 *Mus musculus* neurogenic differentiation fact... 38 4.5
- S66408, S66408 c-erbB=proto-oncogene {exon 1, promoter} [chic... 38 4.5
- AC002396, AC002396 *Arabidopsis thaliana* chromosome I BAC F3I6... 38 4.5
- AE000665, MMAE000665 *Mus musculus* TCR beta locus from bases 5... 38 4.5
- L39837, DROWARTS *Drosophila melanogaster* tumor supressor (war... 38 4.5
- AG000377, AG000377 *Homo sapiens* genomic DNA, 21q region, clo... 38 4.5
- X05632, HSMHCAG1 Human alpha-MHC gene for myosin heavy chain... 38 4.5
- AC002108, AC002108 Genomic sequence from Mouse 4, complete se... 38 4.5
- U37219, HSU37219 Human cyclophilin-like protein CyP-60 mRNA. ... 38 4.5
- M58633, MUSEP58GTA Mouse p58/GTA protein kinase mRNA, complete... 38 4.5
- M25162, HUMMYHC08 Human cardiac alpha-myosin heavy chain (MYH... 38 4.5
- Z46259, SCRPD3COS *S.cerevisiae* FY1676 RPD3 gene. 38 4.5
- U09558, LJU09558 *Lactobacillus johnsonii* ATCC 11506 insertion... 38 4.5
- U66160, MMUSC104 *Mus musculus* extracellular matrix associated... 38 4.5
- Z73126, SCYLL021W *S.cerevisiae* chromosome XII reading frame ... 38 4.5
- U83981, HSU83981 *Homo sapiens* apoptosis associated protein (G... 38 4.5

U59897, MRU59897 *Macropus robustus* hypoxanthine phosphoribosy... 38 4.5  
 D38256, YSCSCT1 Yeast gene for suppressor of ctr mutation 38 4.5  
 X69838, HSG9A *H.sapiens* mRNA for G9a 38 4.5  
 X52952, RNCMOSO Rat mRNA for c-mos 38 4.5  
 U37221, HSU37221 Human cyclophilin-like protein mRNA, partial... 38 4.5  
 X65880, DPRH4OP1 *D.pseudoobscura* rh4 opsin gene, exon 1 38 4.5  
 U58971, NTU58971 *Nicotiana tabacum* calmodulin-binding protein... 38 4.5  
 Z35773, SCYBL012C *S.cerevisiae* chromosome II reading frame O... 38 4.5  
 X67668, MMHMG2 *M.musculus* mRNA for high mobility group 2 pro... 38 4.5  
 L81727, HSL81727 *Homo sapiens* (subclone 1\_d5 from P1 H69) DNA... 38 4.5  
 AL023800, HS833B2 Human DNA sequence \*\*\* SEQUENCING IN PROGR... 38 4.5  
 X62438, HVPERO *H.vulgare* mRNA for peroxidase 38 4.5  
 AC004096, AC004096 Mouse Cosmid ma66a100 from 14D1-D2, comple... 38 4.5  
 AL008980, PFSC03050 *Plasmodium falciparum* DNA \*\*\* SEQUENCING... 38 4.5  
 U64827, MMU64827 *Mus musculus* extracellular matrix associated... 38 4.5  
 AC003010, HUAC003010 *Homo sapiens* Chromosome 16 BAC clone CIT... 38 4.5  
 AE001002, AE001002 *Archaeoglobus fulgidus* section 105 of 172 ... 38 4.5  
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 38 4.5  
 M20386, CHKEGFR Chicken epidermal growth factor receptor (CER... 38 4.5  
 M77637, CHKEGF *Gallus gallus* EGF/TGF-alpha receptor (c-erbB) ... 38 4.5  
 U08185, MMU08185 *Mus musculus* BALB/c zinc-finger protein Blim... 38 4.5  
 AC004231, AC004231 *Homo sapiens* chromosome 17, clone hRPC.111... 38 4.5  
 Z50100, HVC39SAT *H.vulgare* GAA-satellite DNA 38 4.5  
 X53731, SCSPA2G *S. cerevisiae* SPA2 gene 38 4.5  
 U37220, HSU37220 Human cyclophilin-like protein mRNA, partial... 38 4.5  
 X97560, SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome... 38 4.5  
 AB011479, AB011479 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5  
 U89340, LVU89340 *Lytechinus variegatus* Endo16 homolog (LvEndo1... 38 4.5  
 U73850, TCU73850 *Trypanosoma cruzi* 29 kDa proteasome subunit ... 38 4.5  
 AB006698, AB006698 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5  
 D37888, CYIMYC2 *Cyprinus carpio* c-myc gene for c-Myc, comple... 38 4.5  
 AF017349, MMDSGIII 7 *Mus musculus* desmoglein 3 (Dsg3) gene, i... 38 4.5  
 X91807, OSTA136 *O.sativa* mRNA for alpha-tubulin (clone OSTA-... 38 4.5  
 Z71587, SCYNL311C *S.cerevisiae* chromosome XIV reading frame ... 38 4.5  
 AE000742, AE000742 *Aquifex aeolicus* section 74 of 109 of the ... 38 4.5

#### HUMAN ESTs

AA324311, AA324311 EST27136 Cerebellum II *Homo sapiens* cDNA 5... 593 e-167  
 AA639190, AA639190 ns04a01.r1 NCI\_CGAP\_Ew1 *Homo sapiens* cDNA ... 513 e-143  
 AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 505 e-141  
 AA588066, AA588066 nk10d08.s1 NCI\_CGAP\_Co2 *Homo sapiens* cDNA ... 502 e-140  
 AA412036, AA412036 zt68d09.s1 Soares testis NHT *Homo sapiens* ... 502 e-140  
 AA508745, AA508745 ni23a03.s1 NCI\_CGAP\_Co4 *Homo sapiens* cDNA ... 502 e-140

AA480337, AA480337 ne33a03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 502 e-140  
AA902270, AA902270 ok69e04.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 502 e-140  
AA947303, AA947303 ok20d04.s1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Hom... 502 e-140  
R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136  
AA811913, AA811913 ob51d06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 464 e-128  
AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 464 e-128  
AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 400 e-109  
R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 359 5e-97  
AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 315 6e-84  
R58372, R58372 G3243 Fetal heart Homo sapiens cDNA clone G324... 262 8e-68  
AA389703, AA389703 M421 Fetal heart, Lambda ZAP Express Homo ... 202 6e-50  
W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 4e-20  
W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 1e-08  
T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.14  
AA179601, AA179601 zp49f10.r1 Stratagene HeLa cell s3 937216 ... 42 0.14  
AA928679, AA928679 on48e08.s1 NCI\_CGAP\_Co8 Homo sapiens cDNA ... 40 0.55  
AA887972, AA887972 nq95g11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.55  
W46946, W46946 zc40c05.s1 Soares senescent fibroblasts NbHSF ... 40 0.55  
AA887862, AA887862 nq99b08.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.55  
AA554819, AA554819 ni34d08.s1 NCI\_CGAP\_Lu1 Homo sapiens cDNA ... 40 0.55  
AA557362, AA557362 nl81d12.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
AA252258, AA252258 zr29e04.s1 Stratagene NT2 neuronal precurs... 40 0.55  
N34310, N34310 yy52b10.s1 Homo sapiens cDNA clone 277147 3' s... 40 0.55  
AA552228, AA552228 nk06b04.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 40 0.55  
AI017648, AI017648 ou99b02.x1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 40 0.55  
T17395, T17395 NIB846 Normalized infant brain, Bento Soares H... 40 0.55  
AA219659, AA219659 zr05e10.s1 Stratagene NT2 neuronal precurs... 40 0.55  
AA463841, AA463841 zx67f06.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.55  
N66817, N66817 za09b11.s1 Homo sapiens cDNA clone 292029 3' s... 40 0.55  
AA167358, AA167358 zp06f12.s1 Stratagene ovarian cancer (#937... 40 0.55  
AA063505, AA063505 zf70d02.r1 Soares pineal gland N3HPG Homo ... 40 0.55  
AA731625, AA731625 nw64a04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.55  
AA100119, AA100119 zl80g04.s1 Stratagene colon (#937204) Homo... 40 0.55  
AA181572, AA181572 zp51d04.s1 Stratagene HeLa cell s3 937216 ... 40 0.55  
AA327182, AA327182 EST30459 Colon I Homo sapiens cDNA 5' end ... 40 0.55  
R48608, R48608 yj65f07.s1 Homo sapiens cDNA clone 153637 3' s... 40 0.55  
AA678485, AA678485 ah06e04.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
AA082353, AA082353 zn38c11.r1 Stratagene endothelial cell 937... 40 0.55  
AA633213, AA633213 nq57c06.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 40 0.55  
W38410, W38410 zc77g09.s1 Pancreatic Islet Homo sapiens cDNA ... 40 0.55  
AA345893, AA345893 EST51967 Gall bladder I Homo sapiens cDNA ... 40 0.55  
N26876, N26876 yx97f06.s1 Homo sapiens cDNA clone 269699 3' s... 40 0.55  
N95279, N95279 zb60c09.s1 Soares fetal lung NbHL19W Homo sapi... 40 0.55  
AI041637, AI041637 ox92h08.x1 Soares\_senescent\_fibroblasts\_Nb... 40 0.55  
N67830, N67830 za05d12.s1 Homo sapiens cDNA clone 291671 3' s... 40 0.55



AA535094, AA535094 nf84e06.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 AA514414, AA514414 nf57d11.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 T56802, T56802 ya71h07.s2 Homo sapiens cDNA clone 67165 3' co... 40 0.55  
 N68147, N68147 yz55f12.s1 Homo sapiens cDNA clone 286991 3' s... 40 0.55  
 AA535811, AA535811 nf93g10.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 AA115591, AA115591 zl05g09.s1 Soares pregnant uterus NbHPU Ho... 40 0.55  
 N75851, N75851 za96g11.s1 Homo sapiens cDNA clone 300452 3'. 40 0.55  
 AA534433, AA534433 nf80a08.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 H99778, H99778 yx36g01.s1 Homo sapiens cDNA clone 263856 3' s... 40 0.55  
 AA970859, AA970859 oo81h03.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.55  
 F02131, HSC0PF092 H. sapiens partial cDNA sequence; clone c-... 40 0.55  
 AA810279, AA810279 od14g11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.55  
 AA595146, AA595146 nl84b01.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
 AA632386, AA632386 np67e06.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
 AA135124, AA135124 zo24c04.s1 Stratagene colon (#937204) Homo... 40 0.55  
 AA143500, AA143500 zo31b10.s1 Stratagene colon (#937204) Homo... 40 0.55  
 AA854992, AA854992 aj53g12.s1 Soares testis NHT Homo sapiens ... 40 0.55  
 AA156872, AA156872 zl20h07.s1 Soares pregnant uterus NbHPU Ho... 40 0.55  
 AA160994, AA160994 zq41c12.s1 Stratagene hNT neuron (#937233)... 40 0.55  
 AA961724, AA961724 or60a10.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 40 0.55  
 AA551210, AA551210 nj27e09.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA ... 40 0.55  
 R44103, R44103 yg27c10.s1 Homo sapiens cDNA clone 33636 3'. 40 0.55  
 AA938086, AA938086 oj08h08.s1 NCI\_CGAP\_Mel3 Homo sapiens cDNA... 40 0.55  
 AA576021, AA576021 nm57d11.s1 NCI\_CGAP\_Br3 Homo sapiens cDNA ... 40 0.55  
 AA722725, AA722725 zg86b09.s1 Soares fetal heart NbHH19W Homo... 40 0.55  
 AA678948, AA678948 ah08h11.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 W07435, W07435 za96g11.r1 Soares fetal lung NbHL19W Homo sapi... 40 0.55  
 T34639, T34639 EST72167 Homo sapiens cDNA 5' end similar to s... 40 0.55  
 AA632245, AA632245 np67b09.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.55  
 R76418, R76418 yi58a10.s1 Homo sapiens cDNA clone 143418 3'. 40 0.55  
 AI028447, AI028447 ow08b09.x1 Soares\_parathyroid\_tumor\_NbHPA ... 40 0.55  
 AI002929, AI002929 an15e12.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA779388, AA779388 ae26a03.s1 Soares NbHFB Homo sapiens cDNA ... 40 0.55  
 AA776220, AA776220 ah10f02.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA815223, AA815223 oc05c04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.55  
 W60807, W60807 zd27b08.s1 Soares fetal heart NbHH19W Homo sap... 40 0.55  
 AA666007, AA666007 ag71g01.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA643849, AA643849 np26f07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 40 0.55  
 AA846740, AA846740 aj99b12.s1 Soares parathyroid tumor NbHPA ... 40 0.55  
 AA598498, AA598498 ae38h01.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA535972, AA535972 nf95a01.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 AA488544, AA488544 ab37g06.r1 Stratagene HeLa cell s3 937216 ... 40 0.55  
 AA866044, AA866044 oh52g07.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 40 0.55  
 C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.55

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 167 1e-39  
 AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.78  
 AA413261, AA413261 ve52f04.r1 Beddington mouse embryonic regi... 38 0.78  
 AA097645, AA097645 mm36f09.r1 Stratagene mouse skin (#937313)... 38 0.78  
 AA122578, AA122578 mn25b08.r1 Beddington mouse embryonic regi... 38 0.78  
 AA122581, AA122581 mn25c08.r1 Beddington mouse embryonic regi... 38 0.78  
 AA646168, AA646168 vn11e06.r1 Stratagene mouse Tcell 937311 M... 36 3.1  
 AA200881, AA200881 mu03c09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1  
 AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 3.1  
 AA217675, AA217675 mv01b09.r1 Soares mouse lymph node NbMLN M... 36 3.1  
 AI006387, AI006387 ua71d09.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1  
 AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 3.1  
 AA207387, AA207387 mv89a11.r1 GuayWoodford Beier mouse kidney... 36 3.1  
 AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 3.1  
 AA123112, AA123112 mn30g01.r1 Beddington mouse embryonic regi... 36 3.1  
 AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 3.1  
 AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 3.1  
 W12171, W12171 ma59a10.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.1  
 AA208446, AA208446 mv85e01.r1 GuayWoodford Beier mouse kidney... 36 3.1  
 AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 3.1  
 AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 3.1  
 AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 3.1  
 AA561847, AA561847 vl27a12.r1 Stratagene mouse Tcell 937311 M... 36 3.1  
 AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 3.1  
 AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1  
 AA052080, AA052080 mf69f12.r1 Soares mouse embryo NbME13.5 14... 36 3.1  
 AA000646, AA000646 mg23f09.r1 Soares mouse embryo NbME13.5 14... 36 3.1  
 AA510521, AA510521 vh59a05.r1 Soares mouse mammary gland NbMM... 36 3.1  
 AI006122, AI006122 ua86h01.r1 Soares mouse mammary gland NbMM... 36 3.1  
 AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 3.1  
 W77413, W77413 me64d06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1  
 AA114809, AA114809 mn17e09.r1 Beddington mouse embryonic regi... 36 3.1  
 AA793564, AA793564 vn54c05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.1  
 AA174537, AA174537 mt10f09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1  
 W62181, W62181 md87d08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1  
 AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.1  
 AA286005, AA286005 va30e05.r1 GuayWoodford Beier mouse kidney... 36 3.1  
 AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 3.1  
 AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 3.1

AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 44 0.011

AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 C70525, C70525 *C.elegans* cDNA clone yk409g6 : 5' end, single... 44 0.011  
 AA520235, AA520235 TgESTzz53c06.r1 TgME49 invivo Bradyzoite c... 42 0.044  
 T42800, T42800 6063 *Lambda-PRL2 Arabidopsis thaliana* cDNA clo... 42 0.044  
 R29976, R29976 12581 *Lambda-PRL2 Arabidopsis thaliana* cDNA cl... 42 0.044  
 H32045, H32045 EST106774 Rat PC-12 cells, untreated *Rattus* sp... 40 0.18  
 AA819924, AA819924 MF5MA171.AE3 *S. mansoni* female adult Lambd... 40 0.18  
 H37128, H37128 15257 *Lambda-PRL2 Arabidopsis thaliana* cDNA cl... 40 0.18  
 T04367, T04367 414 *Lambda-PRL2 Arabidopsis thaliana* cDNA clon... 40 0.18  
 R90528, R90528 16883 *Lambda-PRL2 Arabidopsis thaliana* cDNA cl... 40 0.18  
 AA660422, AA660422 00298 *MtRHE Medicago truncatula* cDNA 5' 40 0.18  
 U94861, RU94861 *Rattus norvegicus* clone HCY3 mRNA sequence 40 0.18  
 F14275, ATTS5197 *A. thaliana* transcribed sequence; clone YBY... 38 0.69  
 W43730, W43730 23107 CD4-16 *Arabidopsis thaliana* cDNA clone H... 38 0.69  
 N65025, N65025 20065 *Lambda-PRL2 Arabidopsis thaliana* cDNA cl... 38 0.69  
 AI001628, AI001628 EST0210 *Tilapia* brain cDNA library in pUC1... 38 0.69  
 H74687, H74687 383 *Brassica napus* cDNA clone R25R. 38 0.69  
 AA395597, AA395597 27394 *Lambda-PRL2 Arabidopsis thaliana* cDN... 38 0.69  
 AA753070, AA753070 97AS2091 Rice Immature Seed *Lambda* ZAPII c... 38 0.69  
 D41274, RICS3647A Rice cDNA, partial sequence (S3647\_1A). 38 0.69  
 Z25731, ATTS1208 *A. thaliana* transcribed sequence; clone VCV... 38 0.69  
 N82780, N82780 TgESTzy34e03.r1 TgRH Tachyzoite cDNA Toxoplasm... 38 0.69  
 AA597822, AA597822 29889 *Lambda-PRL2 Arabidopsis thaliana* cDN... 38 0.69  
 AA948906, AA948906 LD27590.5prime LD *Drosophila melanogaster* ... 38 0.69  
 AI013695, AI013695 EST208370 Normalized rat spleen, Bento Soa... 38 0.69  
 AA753263, AA753263 96BS0294 Rice Immature Seed *Lambda* ZAPII c... 38 0.69  
 F14402, ATTS5324 *A. thaliana* transcribed sequence; clone TAP... 36 2.7  
 T46158, T46158 9421 *Lambda-PRL2 Arabidopsis thaliana* cDNA clo... 36 2.7  
 C91400, C91400 *Dictyostelium discoideum* slug cDNA, clone SSK169 36 2.7  
 T46009, T46009 9272 *Lambda-PRL2 Arabidopsis thaliana* cDNA clo... 36 2.7  
 AA440655, AA440655 LD15510.5prime LD *Drosophila melanogaster* ... 36 2.7  
 AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A *Schistosom*... 36 2.7  
 Z32623, ATTS2751 *A. thaliana* transcribed sequence; clone YAP... 36 2.7  
 T43683, T43683 6946 *Lambda-PRL2 Arabidopsis thaliana* cDNA clo... 36 2.7  
 AA263535, AA263535 LD06645.5prime LD *Drosophila melanogaster* ... 36 2.7  
 C37095, C37095 *C.elegans* cDNA clone yk482c11 : 3' end, singl... 36 2.7

C57017, C57017 *C.elegans* cDNA clone yk308h9 : 3' end, single... 36 2.7  
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 2.7  
 C92242, C92242 *Dictyostelium discoideum* slug cDNA, clone SSD283 36 2.7  
 Z33976, ATTS3037 *A. thaliana* transcribed sequence; clone YAP... 36 2.7  
 R62091, R62091 EST351 *Strongylocentrotus purpuratus* cDNA 5' end. 36 2.7  
 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 2.7  
 C74456, C74456 Rice cDNA, partial sequence (E31357\_1A) 36 2.7  
 AA753227, AA753227 97AS2316 Rice Immature Seed Lambda ZAPII c... 36 2.7  
 C92456, C92456 *Dictyostelium discoideum* slug cDNA, clone SSE569 36 2.7  
 T20458, T20458 2466 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7  
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7  
 M79841, M79841 wEST00378 *Caenorhabditis elegans* cDNA clone CE... 36 2.7  
 Z17562, ATTS0136 *A. thaliana* transcribed sequence; clone TAT... 36 2.7  
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 2.7  
 T20404, T20404 2412 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7  
 AI012789, AI012789 EST207240 Normalized rat placenta. Bento S... 36 2.7  
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 2.7  
 AA660182, AA660182 00022 MtrHE *Medicago truncatula* cDNA 5' si... 36 2.7  
 D48514, RICS14740A Rice cDNA, partial sequence (S14740\_1A). 36 2.7  
 C90110, C90110 *Dictyostelium discoideum* slug cDNA, clone SSI103 36 2.7  
 H36880, H36880 15009 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7  
 AA699152, AA699152 HL07807.5prime HL *Drosophila melanogaster* ... 36 2.7  
 C11922, C11922 *C.elegans* cDNA clone yk144a11 : 5' end, singl... 36 2.7  
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 2.7

SEQ ID NO:556

X99668, MM22A3 *M.musculus* mRNA for exon from unknown gene 22A3 260 5e-67  
 Z83760, CICOS41 *Ciona intestinalis* DNA sequence from cosmid ... 40 0.94  
 Z75710, CED1081 *Caenorhabditis elegans* cosmid D1081, complet... 40 0.94  
 U73628, HSU73628 Human chromosome 11 101h11 cosmid, complete ... 40 0.94  
 X99757, DMDYDTRO *D.melanogaster* mRNA for dystrophin 38 3.7  
 U51189, HIVU51189 HIV-1 clone 93th253 from Thailand, complete... 38 3.7  
 AC004118, AC004118 *Drosophila melanogaster* (P1 DS06238 (D26))... 38 3.7  
 U50313, CELF44C4 *Caenorhabditis elegans* cosmid F44C4. 38 3.7  
 AC004503, AC004503 *Homo sapiens* chromosome 5, P1 clone 1354A7... 38 3.7  
 M16840, WHTCPA2 Wheat Asp-tRNA gene. 38 3.7  
 Y13381, RNAMPH1 *Rattus norvegicus* mRNA for amphiphysin. amph1 38 3.7  
 AC002994, AC002994 *Homo sapiens* chromosome 17, clone HRPC987K... 38 3.7  
 AB008271, AB008271 *Arabidopsis thaliana* genomic DNA, chromos... 38 3.7  
 D49701, ASNNIAD *Aspergillus oryzae* niaD gene for nitrate red... 38 3.7

X59422, HSPLD1 H.sapiens Pl d1 repetitive DNA 38 3.7  
 Z98555, PFSC03027 Plasmodium falciparum DNA \*\*\* SEQUENCING I... 38 3.7

# HUMAN ESTs

AA315671, AA315671 EST187451 Colon carcinoma (HCC) cell line ... 932 0.0  
 U56653, HSU56653 Human heat shock inducible mRNA 769 0.0  
 AA487685, AA487685 ab23b09.r1 Stratagene lung (#937210) Homo ... 751 0.0  
 AA044797, AA044797 zk67g12.r1 Soares pregnant uterus NbHPU Ho... 749 0.0  
 AA314922, AA314922 EST186735 HCC cell line (matastasis to liv... 698 0.0  
 AA082278, AA082278 zn42d12.r1 Stratagene endothelial cell 937... 668 0.0  
 H22613, H22613 yn64f03.r1 Homo sapiens cDNA clone 173213 5'. 624 e-177  
 AA044743, AA044743 zk67g12.s1 Soares pregnant uterus NbHPU Ho... 622 e-176  
 AA487470, AA487470 ab23b09.s1 Stratagene lung (#937210) Homo ... 601 e-170  
 AA121057, AA121057 zm22b03.r1 Stratagene pancreas (#937208) H... 581 e-164  
 AA194396, AA194396 zq05g05.s1 Stratagene muscle 937209 Homo s... 535 e-150  
 AA384283, AA384283 EST97787 Thyroid Homo sapiens cDNA 5' end 535 e-150  
 AA669015, AA669015 ab88f01.s1 Stratagene lung (#937210) Homo ... 535 e-150  
 AA194336, AA194336 zq05g05.r1 Stratagene muscle 937209 Homo s... 505 e-141  
 R96173, R96173 yt84e09.r1 Homo sapiens cDNA clone 231016 5'. 486 e-135  
 AA028934, AA028934 zk08b09.s1 Soares pregnant uterus NbHPU Ho... 484 e-134  
 AA564849, AA564849 nj22c04.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA ... 442 e-122  
 AA932576, AA932576 oo57g10.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 440 e-121  
 AA876265, AA876265 oi12g09.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 434 e-120  
 AA025525, AA025525 ze86a11.s1 Soares fetal heart NbHH19W Homo... 430 e-118  
 U56654, HSU56654 Human heat shock inducible mRNA 426 e-117  
 AA746600, AA746600 nx18c02.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 406 e-111  
 AA876346, AA876346 oj24a11.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 406 e-111  
 W23082, W23082 78D1 Human retina cDNA Tsp509I-cleaved sublibr... 402 e-110  
 AI034059, AI034059 owl4h11.x1 Soares parathyroid tumor NbHPA ... 357 2e-96  
 AA662934, AA662934 nu92d09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 323 2e-86  
 AA844331, AA844331 ai95f01.s1 Soares parathyroid tumor NbHPA ... 301 8e-80  
 AA249866, AA249866 y0761.seq.F Human fetal heart, Lambda ZAP ... 297 1e-78  
 R19215, R19215 yg24b07.r1 Homo sapiens cDNA clone 33126 5'. 280 3e-73  
 T39355, T39355 ya04g08.r1 Homo sapiens cDNA clone 60542 5'. 254 2e-65  
 AA731264, AA731264 nw57c08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 220 2e-55  
 AA768549, AA768549 oa67c07.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 220 2e-55  
 AA668506, AA668506 ac49a11.s1 Stratagene hNT neuron (#937233)... 216 4e-54  
 T55337, T55337 yb79b05.s1 Homo sapiens cDNA clone 77361 3'. 198 8e-49  
 AA860575, AA860575 aj86a09.s1 Soares parathyroid tumor NbHPA ... 198 8e-49  
 AA335548, AA335548 EST39962 Epididymus Homo sapiens cDNA 5' end 109 6e-22  
 R13183, R13183 yf73f02.r1 Homo sapiens cDNA clone 27960 5'. 58 2e-06  
 T80034, T80034 yd04c06.r1 Homo sapiens cDNA clone 24672 5'. 38 1.8  
 AA595230, AA595230 nl84g02.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 38 1.8

AA871935, AA871935 vq42h02.r1 Barstead bowel MPLRB9 Mus muscu... 664 0.0  
 AA062330, AA062330 ml35e10.r1 Stratagene mouse testis (#93730... 589 e-167  
 AI048164, AI048164 ud71b09.y1 Sugano mouse liver mlia Mus mus... 537 e-151  
 W08037, W08037 mb37h01.r1 Soares mouse p3NMF19.5 Mus musculus... 462 e-128  
 AA387311, AA387311 vc19a03.r1 Ko mouse embryo 11 5dpc Mus mus... 264 6e-69  
 AA163072, AA163072 ms31a11.r1 Stratagene mouse skin (#937313)... 212 2e-53  
 AA596763, AA596763 vm60a10.r1 Stratagene mouse Tcell 937311 M... 178 3e-43  
 AA562549, AA562549 vl63a11.r1 Knowles Solter mouse blastocyst... 143 2e-32  
 AA212378, AA212378 mu44c03.r1 Soares 2NbMT Mus musculus cDNA ... 113 1e-23  
 AA450862, AA450862 vg55h12.r1 Beddington mouse embryonic regi... 111 5e-23  
 AA990073, AA990073 ua59a01.r1 Soares 2NbMT Mus musculus cDNA ... 86 3e-15  
 AA921175, AA921175 vy54b10.r1 Stratagene mouse lung 937302 Mu... 78 8e-13  
 AA261119, AA261119 mz89e01.r1 Soares mouse NML Mus musculus c... 38 0.65  
 AI005952, AI005952 ua80f06.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.6  
 AA123274, AA123274 mn23a08.r1 Beddington mouse embryonic regi... 36 2.6  
 AI036828, AI036828 vw96c02.r1 Stratagene mouse skin (#937313)... 36 2.6

H35787, H35787 EST109178 Rat PC-12 cells, NGF-treated (9 days... 105 3e-21  
 AA686082, AA686082 EST109179 Rat PC-12 cells, NGF-treated (9 ... 86 3e-15  
 C23464, C23464 Jpanese flounder liver cDNA, LE5(10) 72 4e-11  
 C23465, C23465 Jpanese flounder liver cDNA, LE5(10) 56 2e-06  
 AA520314, AA520314 TgESTzz38h12.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 AA520085, AA520085 TgESTzz37g05.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 AA520033, AA520033 TgESTzz36f10.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 AA012516, AA012516 TgESTzz23f04.r1 TgME49cDNA Toxoplasma gond... 38 0.57  
 AA274286, AA274286 TgESTzz24c01.sl TgME49 invivo Bradyzoite c... 38 0.57  
 AA660585, AA660585 00471 MtrHE Medicago truncatula cDNA 5' si... 38 0.57  
 L35828, BNAESTBD Brassica rapa (clone F0621) expressed sequen... 38 0.57  
 AA520070, AA520070 TgESTzz37e05.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 C30080, C30080 C.elegans cDNA clone yk236c3 : 3' end, single... 36 2.3  
 C39044, C39044 C.elegans cDNA clone yk505a4 : 3' end, single... 36 2.3  
 C55023, C55023 C.elegans cDNA clone yk422a3 : 3' end, single... 36 2.3  
 AA542589, AA542589 fa08d06.sl Zebrafish ICRFzfls Danio rerio ... 36 2.3  
 N25370, N25370 EST000480 Schistosoma mansoni cDNA clone SMTBA... 36 2.3  
 AA820625, AA820625 LD24443.5prime LD Drosophila melanogaster ... 36 2.3  
 AA494922, AA494922 fa12g10.r1 Zebrafish ICRFzfls Danio rerio ... 36 2.3  
 AA495181, AA495181 fa04d06.sl Zebrafish ICRFzfls Danio rerio ... 36 2.3  
 D73287, CELK116G6R C.elegans cDNA clone yk116g6 : 3' end, si... 36 2.3  
 C28238, C28238 Rice cDNA, partial sequence (C60429\_1A) 36 2.3

SEQ ID NO:557

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 948 0.0  
 S51239, S51239 calreticulin [Aplysia californica=marine snail... 56 1e-05  
 Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.012  
 U25723, CPU25723 Cavia porcellus alpha-2B adrenoceptor gene, ... 44 0.047  
 AL021407, HS13D10 Homo sapiens DNA sequence from PAC 13D10 o... 42 0.19  
 U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.19  
 V01470, ZMZE01 Zea mays gene encoding a zein gene (clone lam... 42 0.19  
 U06631, HSU06631 Human (H326) mRNA, complete cds. 42 0.19  
 X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.19  
 AE000926, AE000926 Methanobacterium thermoautotrophicum from ... 42 0.19  
 AC004135, AC004135 Genomic sequence for Arabidopsis thaliana ... 42 0.19  
 AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 40 0.74  
 AF050157, MMHC135G15 Mus musculus major histocompatibility lo... 40 0.74  
 AC002352, AC002352 Homo sapiens 12q24 PAC P256D10 complete se... 40 0.74  
 X07699, MMNUCLEO Mouse nucleolin gene 40 0.74  
 X02399, MMHOM6 Mouse embryonal carcinoma DNA fragment contain... 40 0.74  
 M93661, RATNOTCHX Rat notch 2 mRNA. 40 0.74  
 M17440, MUSMHC4H2S Mouse MHC (H-2) S region complement compon... 40 0.74  
 U15972, MMU15972 Mus musculus homeobox (Hoxa7) gene, complete... 40 0.74  
 AB001601, AB001601 Homo sapiens DBP2 mRNA for ATP-dependent ... 40 0.74  
 U09820, HSU09820 Human helicase II (RAD54L) mRNA, complete cds. 40 0.74  
 AB011149, AB011149 Homo sapiens mRNA for KIAA0577 protein, c... 40 0.74  
 U26259, MMU26259 Mus musculus C2-H2 zinc finger protein mRNA,... 40 0.74  
 L48363, MUSZFPTX Mus musculus zinc finger protein gene, compl... 40 0.74  
 AC003113, AC003113 Arabidopsis thaliana BAC F24O1 chromosome ... 40 0.74  
 D76432, D76432 Mouse mRNA for transcriptional repressor delt... 40 0.74  
 U72937, HSU72937 Human putative DNA dependent ATPase and heli... 40 0.74  
 U72915, HSATRX16 Human putative DNA dependent ATPase and heli... 40 0.74  
 U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 0.74  
 Z48618, SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), ... 40 0.74  
 U75653, HSU75653 Human zinc finger helicase (Znf-HX) mRNA. co... 40 0.74  
 Z72672, SCYGL150C S.cerevisiae chromosome VII reading frame ... 40 0.74  
 Z50109, CEC09H10 Caenorhabditis elegans cosmid C09H10, compl... 40 0.74  
 AF013969, AF013969 Mus musculus antigen containing epitope to... 40 0.74  
 M95627, HUMAAMP1X Homo sapiens angio-associated migratory cel... 40 0.74  
 U72936, HSU72936 Human putative DNA dependent ATPase and heli... 40 0.74  
 M88753, DROHTCHRPI Fruitfly heterochromatin protein-1 gene. c... 40 0.74  
 U76906, REU76906 Rhizobium etli FixK (fixK). FixN (fixN). mon... 40 0.74  
 U97085, HSXNP14 Homo sapiens X-linked nuclear protein (ATRX) ... 40 0.74  
 L34363, HUMNUCPRO Human X-linked nuclear protein (XNP) gene. ... 40 0.74  
 U72938, HSU72938 Human putative DNA dependent ATPase and heli... 40 0.74

X56983, EAVATP1 E.arvense gene for catalytic 70kDa V-ATPase ... 40 0.74  
 U88539, MMU88539 Mus musculus chromatin structural protein ho... 40 0.74  
 U07704, HSU07704 Human protein kinase PITSLRE isoform PBETA21... 38 2.9  
 U07705, HSU07705 Human protein kinase PITSLRE isoform PBETA22... 38 2.9  
 AF019612, AF019612 Homo sapiens S2P mRNA, complete cds 38 2.9  
 U04818, HSU04818 Human protein kinase PITSLRE alpha 2-4 mRNA.... 38 2.9  
 AB002381, AB002381 Human mRNA for KIAA0383 gene, partial cds 38 2.9  
 AB009520, AB009520 Pyrococcus horikoshii OT3 genomic DNA, 13... 38 2.9  
 Z83848, HS57A13 Human DNA sequence from PAC 57A13 between ma... 38 2.9  
 AC004592, AC004592 Homo sapiens PAC clone DJ0244J05 from 5q31... 38 2.9  
 L11710, ZEFZCMYC Brachydanio rerio c-myc oncoprotein mRNA, co... 38 2.9  
 D43920, CHKMETASE Chicken mRNA for DNA (cytosine-5-)-methylt... 38 2.9  
 U49056, RNU49056 Rattus norvegicus CTD-binding SR-like protei... 38 2.9  
 U04824, HSU04824 Human protein kinase PITSLRE alpha 2-1 mRNA.... 38 2.9  
 U78045, HSU78045 Human collagenase and stromelysin genes, com... 38 2.9  
 U04816, HSU04816 Human protein kinase PITSLRE alpha 2-2 mRNA.... 38 2.9  
 U04817, HSU04817 Human protein kinase PITSLRE alpha 2-3 mRNA.... 38 2.9

#### HUMAN ESTs

AA639190, AA639190 ns04a01.r1 NCI\_CGAP\_Ew1 Homo sapiens cDNA ... 519 e-145  
 AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 513 e-144  
 R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136  
 AA902270, AA902270 ok69e04.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 450 e-124  
 AA947303, AA947303 ok20d04.s1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Hom... 402 e-110  
 AA588066, AA588066 nk10d08.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 347 1e-93  
 AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 347 1e-93  
 AA480337, AA480337 ne33a03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 347 1e-93  
 AA508745, AA508745 ni23a03.s1 NCI\_CGAP\_Co4 Homo sapiens cDNA ... 347 1e-93  
 AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 315 4e-84  
 AA811913, AA811913 ob51d06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 299 2e-79  
 AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 299 2e-79  
 AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 250 2e-64  
 R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 250 2e-64  
 W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 3e-20  
 W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 6e-09  
 AA737681, AA737681 nw63c04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 42 0.090  
 T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.090  
 R52021, R52021 yg84h09.r1 Homo sapiens cDNA clone 40181 5' si... 42 0.090  
 AA569993, AA569993 nm47h04.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 42 0.090  
 R50149, R50149 yj61c05.s1 Homo sapiens cDNA clone 153224 3' s... 42 0.090  
 R87930, R87930 yo47a11.s1 Homo sapiens cDNA clone 181052 3' s... 42 0.090  
 AA812204, AA812204 ob84f01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 42 0.090  
 AA770224, AA770224 ah82e12.s1 Soares testis NHT Homo sapiens ... 42 0.090



D29591, HUMNK752 Human keratinocyte cDNA, clone 752 40 0.36  
 AA324325, AA324325 EST27219 Cerebellum II Homo sapiens cDNA 5... 40 0.36  
 AA053063, AA053063 zl71c03.r1 Stratagene colon (#937204) Homo... 40 0.36  
 T35539, T35539 EST86964 Homo sapiens cDNA 5' end similar to N... 40 0.36  
 AA974278, AA974278 oq14d03.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 40 0.36  
 W26196, W26196 22b5 Human retina cDNA randomly primed sublibr... 40 0.36  
 H92585, H92585 yt89c03.s1 Homo sapiens cDNA clone 231460 3'. 40 0.36  
 AA232334, AA232334 zr27b04.r1 Stratagene NT2 neuronal precurs... 40 0.36  
 N55775, N55775 J2481F Homo sapiens cDNA clone J2481 5'. 40 0.36  
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.36  
 C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.36  
 H19156, H19156 yn50c01.r1 Homo sapiens cDNA clone 171840 5'. 40 0.36  
 AA299557, AA299557 EST12080 Uterus tumor I Homo sapiens cDNA ... 40 0.36  
 W84460, W84460 zd89d12.r1 Soares fetal heart NbHH19W Homo sap... 40 0.36  
 T54194, T54194 ya90a02.r2 Homo sapiens cDNA clone 68906 5'. 40 0.36  
 AA100203, AA100203 zm16f12.r1 Stratagene pancreas (#937208) H... 38 1.4  
 AA993061, AA993061 ot92h08.s1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 38 1.4  
 R53406, R53406 yj70d07.r1 Homo sapiens cDNA clone 154093 5' s... 38 1.4  
 H99671, H99671 yx35b03.s1 Homo sapiens cDNA clone 263693 3'. 38 1.4  
 W03410, W03410 za07c09.r1 Soares melanocyte 2NbHM Homo sapien... 38 1.4  
 N35475, N35475 yy24b03.s1 Homo sapiens cDNA clone 272141 3'. 38 1.4  
 AA630851, AA630851 nt57f04.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA ... 38 1.4  
 N66458, N66458 yz41b08.s1 Homo sapiens cDNA clone 285591 3'. 38 1.4  
 AA736438, AA736438 zh31b09.s1 Soares pineal gland N3HPG Homo ... 38 1.4  
 AA911761, AA911761 og19b01.s1 NCI\_CGAP\_PNS1 Homo sapiens cDNA... 38 1.4  
 AA085513, AA085513 zn43a10.r1 Stratagene HeLa cell s3 937216 ... 38 1.4  
 AA678530, AA678530 ah02e05.s1 Gessler Wilms tumor Homo sapien... 38 1.4  
 AA782011, AA782011 ai75b12.s1 Soares testis NHT Homo sapiens ... 38 1.4  
 F12352, HSC38H091 H. sapiens partial cDNA sequence; clone c-... 38 1.4  
 AA861288, AA861288 ak33g01.s1 Soares testis NHT Homo sapiens ... 38 1.4  
 AA908705, AA908705 ol01b09.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 1.4  
 AA298850, AA298850 EST114450 Thyroid Homo sapiens cDNA 5' end 38 1.4

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 172 1e-41  
 AI047347, AI047347 ud65c01.y1 Sugano mouse liver mlia Mus mus... 42 0.032  
 AA832736, AA832736 vw45g10.r1 Soares mouse mammary gland NbMM... 42 0.032  
 AA960471, AA960471 vw63a05.s1 Soares mouse mammary gland NMLM... 40 0.13  
 AA880584, AA880584 vw92e01.r1 Stratagene mouse skin (#937313)... 40 0.13  
 AA107508, AA107508 mp05e07.r1 Life Tech mouse embryo 8 5dpc 1... 40 0.13  
 AA116682, AA116682 mn28c06.r1 Beddington mouse embryonic regi... 40 0.13  
 AA522310, AA522310 vi45b02.r1 Beddington mouse embryonic regi... 40 0.13  
 AA162231, AA162231 mn44h02.r1 Beddington mouse embryonic regi... 40 0.13

AA414037, AA414037 vc68g03.s1 Knowles Solter mouse 2 cell Mus... 40 0.13  
 AA596585, AA596585 vm58e12.r1 Stratagene mouse Tcell 937311 M... 38 0.51  
 AA863563, AA863563 vx05a10.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.51  
 AA795177, AA795177 vq94g04.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA914764, AA914764 vy92h04.r1 Soares mouse mammary gland NbMM... 38 0.51  
 AA590440, AA590440 vm20c04.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA260352, AA260352 va93c10.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.51  
 AA444734, AA444734 ve75d10.r1 Soares mouse mammary gland NbMM... 38 0.51  
 C85885, C85885 Mus musculus fertilized egg cDNA 3'-end seque... 38 0.51  
 AA794590, AA794590 vu78h12.r1 Stratagene mouse skin (#937313)... 38 0.51  
 AA529643, AA529643 vi38a09.r1 Beddington mouse embryonic regi... 38 0.51  
 AA607084, AA607084 vm84a09.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA636994, AA636994 vn05g06.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA675676, AA675676 vr73h08.s1 Knowles Solter mouse 2 cell Mus... 38 0.51  
 AA163890, AA163890 ms52f09.r1 Life Tech mouse embryo 13 5dpc ... 38 0.51  
 C80539, C80539 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 38 0.51  
 AA051352, AA051352 mj53a09.r1 Soares mouse embryo NbME13.5 14... 38 0.51  
 W36885, W36885 mb64f09.r1 Soares mouse p3NMF19.5 Mus musculus... 38 0.51  
 AA930627, AA930627 vy67c05.r1 Stratagene mouse macrophage (#9... 38 0.51  
 AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 2.0  
 AA967267, AA967267 vz70e08.r1 Soares mouse mammary gland NbMM... 36 2.0  
 AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 2.0  
 AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 2.0  
 AA170036, AA170036 ms52d01.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0  
 AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 2.0  
 AA555634, AA555634 vk49f08.r1 Stratagene mouse Tcell 937311 M... 36 2.0  
 AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 2.0  
 AA606813, AA606813 vm90h12.r1 Knowles Solter mouse blastocyst... 36 2.0  
 AA591610, AA591610 vk49d08.r1 Stratagene mouse Tcell 937311 M... 36 2.0  
 AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 2.0  
 AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 2.0  
 AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 2.0  
 AA612185, AA612185 vo03d05.r1 Stratagene mouse skin (#937313)... 36 2.0  
 AA103424, AA103424 mo21e05.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0  
 AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.0  
 AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.0  
 AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 2.0  
 AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 2.0  
 AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 2.0  
 AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 2.0  
 AA655241, AA655241 vq84c07.s1 Knowles Solter mouse 2 cell Mus... 36 2.0  
 AA512835, AA512835 vg13f11.r1 Soares mouse NbMH Mus musculus ... 36 2.0

C70525, C70525 *C.elegans* cDNA clone yk409g6 : 5' end, single... 44 0.007  
 F15112, SSO4D09 *S.scrofa* mRNA; expressed sequence tag (5'; c... 42 0.029  
 AA684640, AA684640 EST104989 Rat PC-12 cells, untreated Rattu... 40 0.11  
 H32045, H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 40 0.11  
 AA660422, AA660422 00298 *MtRHE* *Medicago truncatula* cDNA 5' 40 0.11  
 C59696, C59696 *C.elegans* cDNA clone yk440e1 : 3' end, single... 38 0.45  
 AI008699, AI008699 EST203150 Normalized rat embryo, Bento Soa... 38 0.45  
 AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.45  
 T38461, T38461 EST103957 *Saccharomyces cerevisiae* cDNA 3' end. 38 0.45  
 C59257, C59257 *C.elegans* cDNA clone yk386b12 : 3' end, singl... 38 0.45  
 AA948906, AA948906 LD27590.5prime LD *Drosophila melanogaster* ... 38 0.45  
 AI001628, AI001628 EST0210 *Tilapia* brain cDNA library in pUC1... 38 0.45  
 H31962, H31962 EST106545 Rat PC-12 cells, untreated Rattus sp... 38 0.45  
 AA979509, AA979509 LD34118.5prime LD *Drosophila melanogaster* ... 38 0.45  
 D41274, RICS3647A Rice cDNA, partial sequence (S3647\_1A). 38 0.45  
 C58362, C58362 *C.elegans* cDNA clone yk366a8 : 3' end, single... 38 0.45  
 C57756, C57756 *C.elegans* cDNA clone yk298b9 : 3' end, single... 38 0.45  
 AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.45  
 H74687, H74687 383 *Brassica napus* cDNA clone R25R. 38 0.45  
 C10513, C10513 *C.elegans* cDNA clone yk147e9 : 3' end, single... 38 0.45  
 C55569, C55569 *C.elegans* cDNA clone yk191d1 : 3' end, single... 38 0.45  
 C94819, C94819 *Sus scrofa* mRNA; expressed sequence tag (5'; ... 38 0.45  
 C32982, C32982 *C.elegans* cDNA clone yk338a12 : 3' end, singl... 38 0.45  
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 1.8  
 AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA660182, AA660182 00022 *MtRHE* *Medicago truncatula* cDNA 5' si... 36 1.8  
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 1.8  
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 1.8  
 AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 1.8  
 AA440655, AA440655 LD15510.5prime LD *Drosophila melanogaster* ... 36 1.8  
 AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A *Schistosom*... 36 1.8  
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 1.8  
 AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 T46158, T46158 9421 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 1.8  
 AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 Z17562, ATTS0136 *A. thaliana* transcribed sequence: clone TAT... 36 1.8  
 AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 1.8  
 AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 36 1.8  
 C37095, C37095 *C.elegans* cDNA clone yk482c11 : 3' end, singl... 36 1.8

T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8  
 T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8  
 F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 1.8  
 T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8  
 AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 1.8  
 AA902065, AA902065 NCM1A12T3 Mycelial Neurospora crassa cDNA ... 36 1.8

## SEQ ID NO:558

AF016585, AF016585 Streptomyces caelestis cytochrome P-450 hy... 42 0.092  
 U50719, MSU50719 Manduca sexta neuroglian mRNA, complete cds 40 0.36  
 Z97208, SPAC15A10 S.pombe chromosome I cosmid c15A10 40 0.36  
 AC003063, AC003063 Mus musculus Chromosome 16 BAC Clone b40-o... 40 0.36  
 X66455, MMFGFR2 M.musculus promoter region of fibroblast gro... 40 0.36  
 D83785, D83785 Human mRNA for KIAA0200 gene, complete cds 40 0.36  
 AC000398, AC000398 Genomic sequence from Mouse 11, complete s... 38 1.4  
 AF062345, AF062345 Caulobacter crescentus Sts1 (sts1), S-laye... 38 1.4  
 X12359, RCNIFR12 Rhodobacter capsulatus nifR1 and nifR2 gene 38 1.4  
 X72382, RCNIFR3 R.capsulatus nifR3 DNA 38 1.4

## HUMAN ESTs

R36714, R36714 yh93g06.s1 Homo sapiens cDNA clone 137338 3'. 775 0.0  
 D61030, HUM149A04B Human fetal brain cDNA 5'-end GEN-149A04. 666 0.0  
 D60944, HUM141D02B Human fetal brain cDNA 5'-end GEN-141D02. 656 0.0  
 H03308, H03308 yj47d09.s1 Homo sapiens cDNA clone 151889 3'. 609 e-172  
 AA435561, AA435561 zt73d09.s1 Soares testis NHT Homo sapiens ... 587 e-166  
 AA977877, AA977877 oq56d03.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 571 e-161  
 AA846787, AA846787 aj41h03.s1 Soares testis NHT Homo sapiens ... 563 e-159  
 AA972542, AA972542 oo82e01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 561 e-158  
 AA954270, AA954270 on72e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 557 e-157  
 AA740333, AA740333 ob23c02.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 557 e-157  
 AA999722, AA999722 ov04c06.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 555 e-156  
 AA970621, AA970621 op40h08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 551 e-155  
 AA932930, AA932930 oo04g11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 541 e-152  
 AA725406, AA725406 ai13b11.s1 Soares parathyroid tumor NbHPA ... 539 e-152  
 W74439, W74439 zd75d10.s1 Soares fetal heart NbHH19W Homo sap... 539 e-152  
 AA868538, AA868538 ak43e08.s1 Soares testis NHT Homo sapiens ... 539 e-152  
 R79832, R79832 yi89b08.s1 Homo sapiens cDNA clone 146391 3' s... 537 e-151

R63227, R63227 yi07e06.s1 Homo sapiens cDNA clone 138562 3'. 535 e-150  
 AI027967, AI027967 ov84d04.x1 Soares\_testis\_NHT Homo sapiens ... 535 e-150  
 AA776717, AA776717 ah49d07.s1 Soares testis NHT Homo sapiens ... 535 e-150  
 AI040961, AI040961 ov53d06.x1 Soares\_testis\_NHT Homo sapiens ... 533 e-150  
 AI024835, AI024835 ov35h09.x1 Soares\_testis\_NHT Homo sapiens ... 533 e-150  
 AA740667, AA740667 ob01g12.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 531 e-149  
 AA994527, AA994527 ou42h06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 531 e-149  
 AA932728, AA932728 oo31g06.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 529 e-149  
 AI001978, AI001978 ot39f03.s1 Soares\_testis\_NHT Homo sapiens ... 529 e-149  
 N37092, N37092 yy41g08.s1 Homo sapiens cDNA clone 273854 3'. 529 e-149  
 N27547, N27547 yy01e05.s1 Homo sapiens cDNA clone 269984 3'. 527 e-148  
 AA883578, AA883578 al46b08.s1 Soares NFL T GBC S1 Homo sapien... 527 e-148  
 AA890154, AA890154 al53f07.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 525 e-147  
 AA757222, AA757222 ah56f11.s1 Soares testis NHT Homo sapiens ... 525 e-147  
 AA456074, AA456074 aa17b07.s1 Soares NhHMPu S1 Homo sapiens c... 523 e-147  
 AA884285, AA884285 am32f04.s1 Soares NFL T GBC S1 Homo sapien... 523 e-147  
 AA969436, AA969436 op53e12.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 521 e-146  
 AA952918, AA952918 on55h11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 521 e-146  
 AA971938, AA971938 op88b01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 521 e-146  
 R25112, R25112 yh36b12.s1 Homo sapiens cDNA clone 131807 3'. 519 e-146  
 AA865258, AA865258 og87d08.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 519 e-146  
 AA758323, AA758323 ah65e11.s1 Soares testis NHT Homo sapiens ... 519 e-146  
 AA972041, AA972041 op88e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 519 e-146  
 R76443, R76443 yi58e11.s1 Homo sapiens cDNA clone 143468 3'. 519 e-146  
 AA917965, AA917965 om37e04.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 517 e-145  
 AA505880, AA505880 ni01a09.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 517 e-145  
 AA906270, AA906270 oj98e12.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 517 e-145  
 AA758549, AA758549 ah70b04.s1 Soares testis NHT Homo sapiens ... 517 e-145  
 AA927156, AA927156 om20f05.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 515 e-144  
 AA976254, AA976254 oo30f08.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 515 e-144  
 R23891, R23891 yh28a12.s1 Homo sapiens cDNA clone 131038 3'. 515 e-144  
 AA938552, AA938552 oo78g11.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 513 e-144  
 AA483809, AA483809 ne41c08.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 513 e-144  
 AA962659, AA962659 or31f10.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 511 e-143  
 AA724803, AA724803 ai05f02.s1 Soares parathyroid tumor NbHPA ... 511 e-143  
 AA410432, AA410432 zv12c09.s1 Soares NhHMPu S1 Homo sapiens c... 511 e-143  
 AA775373, AA775373 ad19c07.s1 Soares NbHFB Homo sapiens cDNA ... 511 e-143  
 AA758038, AA758038 ah67h09.s1 Soares testis NHT Homo sapiens ... 509 e-143  
 AA904368, AA904368 ol15d02.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 509 e-143  
 AA861386, AA861386 ak37b11.s1 Soares testis NHT Homo sapiens ... 507 e-142  
 R31547, R31547 yh72g03.s1 Homo sapiens cDNA clone 135316 3'. 505 e-141  
 AA843421, AA843421 ak07f11.s1 Soares parathyroid tumor NbHPA ... 504 e-141  
 H02479, H02479 yj35e10.s1 Homo sapiens cDNA clone 150762 3'. 504 e-141  
 N29346, N29346 yw85c12.s1 Homo sapiens cDNA clone 259030 3'. 504 e-141  
 AA815351, AA815351 ai63g05.s1 Soares testis NHT Homo sapiens ... 504 e-141

AA923373, AA923373 ol46e03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 502 e-140  
H01218, H01218 yj31c08.s1 Homo sapiens cDNA clone 150350 3'. 500 e-140  
AA988977, AA988977 or87e11.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 500 e-140  
AA628621, AA628621 af40c02.s1 Soares total fetus Nb2HF8 9w Ho... 500 e-140  
AA442745, AA442745 zv60a07.s1 Soares testis NHT Homo sapiens ... 498 e-139  
AA777492, AA777492 zj02e07.s1 Soares fetal liver spleen 1NFLS... 498 e-139  
R73670, R73670 yi55f03.s1 Homo sapiens cDNA clone 143165 3'. 498 e-139  
H12460, H12460 yj12d05.s1 Homo sapiens cDNA clone 148521 3'. 498 e-139  
AA875917, AA875917 oj15a08.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 496 e-138  
R76230, R76230 yi71g11.s1 Homo sapiens cDNA clone 144740 3'. 494 e-138  
AA970616, AA970616 op40h03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 494 e-138  
AA912408, AA912408 ol23a05.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 492 e-137  
AA910051, AA910051 ol40e08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 492 e-137  
AA815444, AA815444 ai65b11.s1 Soares testis NHT Homo sapiens ... 492 e-137  
R76814, R76814 yi62f06.s1 Homo sapiens cDNA clone 143843 3'. 488 e-136  
AA954722, AA954722 oo84c12.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 488 e-136  
R65987, R65987 yi23e10.s1 Homo sapiens cDNA clone 140106 3'. 486 e-136  
R63480, R63480 yi08e11.s1 Homo sapiens cDNA clone 138668 3'. 486 e-136  
AA885425, AA885425 am12h09.s1 Soares NFL T GBC S1 Homo sapien... 486 e-136  
AA884231, AA884231 am32a01.s1 Soares NFL T GBC S1 Homo sapien... 484 e-135  
AA885048, AA885048 am11a12.s1 Soares NFL T GBC S1 Homo sapien... 482 e-134  
AA996162, AA996162 os14f10.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 482 e-134  
AA748637, AA748637 ny10a02.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 482 e-134  
AI031908, AI031908 ow47e12.x1 Soares\_parathyroid\_tumor\_NbHPA ... 482 e-134  
AA884703, AA884703 am18e02.s1 Soares NFL T GBC S1 Homo sapien... 480 e-134  
AA928243, AA928243 on87c10.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 480 e-134  
AI025986, AI025986 ow03a09.s1 Soares\_parathyroid\_tumor\_NbHPA ... 478 e-133  
AA897637, AA897637 oj72g07.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 472 e-131  
AA877346, AA877346 01c07.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 472 e-131  
AA833569, AA833569 aj46b02.s1 Soares testis NHT Homo sapiens ... 472 e-131  
AA832163, AA832163 oc91b02.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 470 e-131  
R89052, R89052 ym99e08.s1 Homo sapiens cDNA clone 167078 3'. 470 e-131  
N26589, N26589 yx91f03.s1 Homo sapiens cDNA clone 269117 3'. 460 e-128  
R73883, R73883 yi56c03.s1 Homo sapiens cDNA clone 143236 3'. 454 e-126  
AA579968, AA579968 ng51c03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 444 e-123  
AA843427, AA843427 ak07g06.s1 Soares parathyroid tumor NbHPA ... 438 e-121  
AA705903, AA705903 ah42g12.s1 Soares testis NHT Homo sapiens ... 436 e-121  
AA835882, AA835882 oc81d05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 434 e-120  
AA812583, AA812583 aj43b02.s1 Soares testis NHT Homo sapiens ... 432 e-119  
AA512970, AA512970 nj16b08.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 432 e-119  
R26664, R26664 yh35g10.s1 Homo sapiens cDNA clone 131778 3'. 428 e-118  
AA429715, AA429715 zv60a07.r1 Soares testis NHT Homo sapiens ... 414 e-114  
H17430, H17430 ym40f09.s1 Homo sapiens cDNA clone 50607 3'. 404 e-111  
AA436117, AA436117 zu03d10.r1 Soares testis NHT Homo sapiens ... 402 e-110  
AA099077, AA099077 zl77a09.s1 Stratagene colon (#937204) Homo... 400 e-110

R72440, R72440 yj90h02.s1 Homo sapiens cDNA clone 156051 3'. 379 e-103  
 AA577436, AA577436 nm96h06.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 351 4e-95  
 AA516390, AA516390 nf55e03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 347 6e-94  
 AA534533, AA534533 nf80h06.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 341 3e-92  
 AA541583, AA541583 ni89f05.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 311 3e-83  
 N72191, N72191 yz99f07.s1 Homo sapiens cDNA clone 291205 3'. 303 8e-81  
 AA905015, AA905015 ok09b08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 303 8e-81  
 AA393148, AA393148 zt73d09.r1 Soares testis NHT Homo sapiens ... 287 4e-76  
 AA939048, AA939048 op56h04.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 256 2e-66  
 AA412317, AA412317 zt97c05.r1 Soares testis NHT Homo sapiens ... 246 2e-63  
 R65986, R65986 yi23e10.r1 Homo sapiens cDNA clone 140106 5'. 238 4e-61  
 AA400827, AA400827 zt76c07.s1 Soares testis NHT Homo sapiens ... 232 2e-59  
 W00472, W00472 yz99f07.r1 Homo sapiens cDNA clone 291205 5'. 180 8e-44  
 AA860558, AA860558 aj81e09.s1 Soares parathyroid tumor NbHPA ... 180 8e-44  
 AA455577, AA455577 aa17b07.r1 Soares NhHMPu S1 Homo sapiens c... 176 1e-42  
 AA583931, AA583931 nn64e04.s1 NCI\_CGAP\_Lar1 Homo sapiens cDNA... 172 2e-41  
 AA907332, AA907332 ol22g11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 168 3e-40  
 R71169, R71169 yi53a12.r1 Homo sapiens cDNA clone 142942 5'. 159 3e-37  
 W79084, W79084 zd75d10.r1 Soares fetal heart NbHH19W Homo sap... 155 4e-36  
 AA295914, AA295914 EST101137 Thymus III Homo sapiens cDNA 5' end 135 4e-30  
 AA860415, AA860415 aj60d10.s1 Soares testis NHT Homo sapiens ... 100 2e-19  
 H01351, H01351 yi99a07.r1 Homo sapiens cDNA clone 147348 5'. 98 9e-19  
 AA709286, AA709286 ai21g07.s1 Soares testis NHT Homo sapiens ... 96 3e-18  
 AA931370, AA931370 oo03d01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 96 3e-18  
 AA501911, AA501911 ng54a08.s1 NCI\_CGAP\_Li2 Homo sapiens cDNA ... 94 1e-17  
 AA548419, AA548419 nj14g09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 92 5e-17  
 AA588892, AA588892 no23b06.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 92 5e-17  
 AI025228, AI025228 ov40h08.x1 Soares\_testis\_NHT Homo sapiens ... 76 3e-12  
 R73757, R73757 yi55f03.r1 Homo sapiens cDNA clone 143165 5'. 74 1e-11  
 R23710, R23710 yh35g10.r1 Homo sapiens cDNA clone 131778 5'. 56 3e-06  
 N40362, N40362 yy01e05.r1 Homo sapiens cDNA clone 269984 5'. 50 2e-04  
 H59895, H59895 yr04c12.r1 Homo sapiens cDNA clone 204310 5'. 48 7e-04  
 H12509, H12509 yj12d05.r1 Homo sapiens cDNA clone 148521 5'. 44 0.011  
 N20344, N20344 yx38d02.s1 Homo sapiens cDNA clone 264003 3'. 38 0.70  
 AA614692, AA614692 np52b10.s1 NCI\_CGAP\_Br1.1 Homo sapiens cDN... 38 0.70  
 H30707, H30707 yo78f07.r1 Homo sapiens cDNA clone 184069 5'. 36 2.7  
 H52973, H52973 yq82e04.r1 Homo sapiens cDNA clone 202302 5'. 36 2.7  
 AA218550, AA218550 zq96b02.r1 Stratagene NT2 neuronal precurs... 36 2.7  
 AA312481, AA312481 EST183215 Jurkat T-cells VI Homo sapiens c... 36 2.7  
 AA632009, AA632009 np74c07.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 36 2.7  
 H13363, H13363 yl71b10.r1 Homo sapiens cDNA clone 43343 5'. 36 2.7  
 AI022018, AI022018 ow64d01.x1 Soares\_senescent\_fibroblasts\_Nb... 36 2.7  
 AA781996, AA781996 ai75a06.s1 Soares testis NHT Homo sapiens ... 36 2.7  
 N21623, N21623 yx60a09.s1 Homo sapiens cDNA clone 266104 3'. 36 2.7  
 AA326194, AA326194 EST29340 Cerebellum II Homo sapiens cDNA 5... 36 2.7

C76071, C76071 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 250 4e-65  
 AA051612, AA051612 mj52c07.r1 Soares mouse embryo NbME13.5 14... 238 1e-61  
 AA561635, AA561635 vl01h07.r1 Knowles Solter mouse blastocyst... 234 2e-60  
 AA288419, AA288419 vb14h01.r1 Soares mouse NML Mus musculus c... 220 3e-56  
 AA212883, AA212883 mw78e10.r1 Soares mouse NML Mus musculus c... 220 3e-56  
 AA268018, AA268018 vb08e07.r1 Soares mouse NML Mus musculus c... 212 8e-54  
 AA692427, AA692427 vt59b07.r1 Barstead mouse irradiated colon... 200 3e-50  
 W18566, W18566 mb98h02.r1 Soares mouse p3NMF19.5 Mus musculus... 192 7e-48  
 AA543948, AA543948 vj69b08.r1 Knowles Solter mouse blastocyst... 147 4e-34  
 W41070, W41070 mc39b06.r1 Soares mouse p3NMF19.5 Mus musculus... 123 5e-27  
 Z31174, MMTEST52 M.musculus expressed sequence tag MTEST52 117 3e-25  
 AA530723, AA530723 vj32f07.r1 Stratagene mouse diaphragm (#93... 74 5e-12  
 AA966940, AA966940 ua38c01.r1 Soares mouse mammary gland NbMM... 72 2e-11  
 AA111079, AA111079 mp50e01.r1 Barstead MPLRB1 Mus musculus cD... 44 0.004  
 AA049187, AA049187 mj51a02.r1 Soares mouse embryo NbME13.5 14... 36 0.99  
 AA058246, AA058246 mg74e12.r1 Soares mouse embryo NbME13.5 14... 36 0.99  
 AA153730, AA153730 mq60a02.r1 Soares 2NbMT Mus musculus cDNA ... 36 0.99  
 AA473959, AA473959 vd02b12.s1 Knowles Solter mouse 2 cell Mus... 36 0.99  
 W47887, W47887 mc83h09.r1 Soares mouse embryo NbME13.5 14.5 M... 36 0.99  
 AA033312, AA033312 mi43g01.r1 Soares mouse embryo NbME13.5 14... 36 0.99  
 AA980820, AA980820 ua46a04.r1 Soares mouse mammary gland NbMM... 36 0.99  
 Z31139, MMTEST427 M.musculus expressed sequence tag MTEST427 36 0.99  
 C76637, C76637 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 34 3.9  
 AI049314, AI049314 uc87b10.y1 Sugano mouse kidney mkia Mus mu... 34 3.9  
 AA670807, AA670807 vs70b02.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA727571, AA727571 vv01h11.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA571966, AA571966 vg12f07.r1 Soares mouse NbMH Mus musculus ... 34 3.9  
 W37059, W37059 mb73f10.r1 Soares mouse p3NMF19.5 Mus musculus... 34 3.9  
 AA760280, AA760280 vv74h11.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA799036, AA799036 vn40c12.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA432831, AA432831 vf28g07.r1 Knowles Solter mouse 8 cell Mus... 34 3.9  
 AA562435, AA562435 vk98c01.r1 Knowles Solter mouse blastocyst... 34 3.9  
 AA726680, AA726680 vu93g12.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA217464, AA217464 mu87d11.r1 Soares mouse lymph node NbMLN M... 34 3.9  
 AA790564, AA790564 vx71e06.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA033172, AA033172 mi37f06.r1 Soares mouse embryo NbME13.5 14... 34 3.9  
 AA616204, AA616204 vo96h02.r1 Soares mouse mammary gland NbMM... 34 3.9  
 AA982055, AA982055 ua37h05.r1 Soares mouse mammary gland NbMM... 34 3.9  
 W47850, W47850 mc82h10.r1 Soares mouse embryo NbME13.5 14.5 M... 34 3.9  
 AA537538, AA537538 vk48c12.r1 Soares mouse mammary gland NbMM... 34 3.9  
 AA636986, AA636986 vn05f04.r1 Knowles Solter mouse blastocyst... 34 3.9



AI043768, AI043768 UI-R-C0-jm-d-11-0-UI.s1 UI-R-C0 Rattus nor... 174 1e-42  
 AA531635, AA531635 TgESTzz29b08.r1 TgME49 invivo Bradyzoite c... 38 0.22  
 AA944260, AA944260 EST199759 Normalized rat embryo, Bento Soa... 38 0.22  
 AI008930, AI008930 EST203381 Normalized rat embryo, Bento Soa... 36 0.87  
 D15788, RICC1258A Rice cDNA, partial sequence (C1258A). 36 0.87  
 AA963741, AA963741 UI-R-C0-gt-b-09-0-UI.s1 UI-R-C0 Rattus nor... 36 0.87  
 AA951235, AA951235 LD31601.3prime LD Drosophila melanogaster ... 34 3.5  
 C20118, C20118 Rice cDNA, partial sequence (E11542\_2A) 34 3.5  
 AA820317, AA820317 LD23876.5prime LD Drosophila melanogaster ... 34 3.5  
 AA950448, AA950448 LD30237.3prime LD Drosophila melanogaster ... 34 3.5

# SEQ ID NO:559

U83883, RNU83883 Rattus norvegicus p105 coactivator mRNA, com... 42 0.11  
 V00722, MMBGL1 Mouse gene for beta-1-globin. 40 0.45  
 X14061, MMBGCXD M.musculus beta-globin complex DNA for y, bh... 40 0.45  
 U20824, EHVU20824 Equine herpesvirus 2, complete genome 38 1.8  
 U04106, PFU04106 Pleurotus fossulatus D1822, mating group VI,... 38 1.8  
 U04101, POU04101 Pleurotus ostreatus D1742, Japan. mating gro... 38 1.8  
 AC005174, AC005174 Homo sapiens clone UWGC:g1564a012 from 7p1... 38 1.8  
 M18680, HUMRGAPS Homo sapiens 5S rRNA pseudogene. 38 1.8  
 AL022121, MTV025 Mycobacterium tuberculosis H37Rv complete g... 38 1.8  
 AF038379, AF038379 Leishmania amazonensis ribosomal protein S... 38 1.8  
 Z11528, THIGPMR T.harzianum mRNA for imidazoleglycerolphosphate 38 1.8  
 U32622, CTU32622 Comamonas testosteroni TsaR (tsaR), toluenes... 38 1.8  
 U04102, POU04102 Pleurotus ostreatus D1743, Japan, mating gro... 38 1.8  
 U04105, PFU04105 Pleurotus fossulatus D1821, mating group VI,... 38 1.8  
 U04109, PEU04109 Pleurotus eryngii D1832, mating group VI rib... 38 1.8  
 U65606, BSU65606 Basidiomycete from a bamboo (Phyllostachys p... 38 1.8

# HUMAN ESTs

R49969, R49969 yj56c07.s1 Homo sapiens cDNA clone 152748 3' s... 523 e-147  
 AA834501, AA834501 of21c02.s1 NCI\_CGAP\_Kid6 Homo sapiens cDNA... 381 e-104  
 W96422, W96422 ze43a05.s1 Soares retina N2b4HR Homo sapiens c... 315 2e-84  
 R47821, R47821 yj56c07.r1 Homo sapiens cDNA clone 152748 5'. 214 7e-54  
 AA761660, AA761660 nz24b09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 212 3e-53  
 AA887861, AA887861 nq99b07.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 74 2e-11  
 AA644044, AA644044 nm20b12.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 72 6e-11

AA115963, AA115963 zm78d11.s1 Stratagene neuroepithelium (#93... 40 0.22  
 AA779271, AA779271 zj43f02.s1 Soares fetal liver spleen 1NFLS... 40 0.22  
 T65600, T65600 yc76a04.r1 Homo sapiens cDNA clone 21496 5'. 38 0.86  
 AA515882, AA515882 nf67f10.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 38 0.86  
 AA664812, AA664812 nu69b05.s1 NCI\_CGAP\_Alv1 Homo sapiens cDNA... 36 3.4  
 T83365, T83365 ye03f05.s1 Homo sapiens cDNA clone 116673 3'. 36 3.4  
 AA009773, AA009773 zi04d04.s1 Soares fetal liver spleen 1NFLS... 36 3.4  
 AA916894, AA916894 og34g10.s1 NCI\_CGAP\_Br7 Homo sapiens cDNA ... 36 3.4  
 N27865, N27865 yy02g03.s1 Homo sapiens cDNA clone 270100 3'. 36 3.4  
 AA953544, AA953544 om79g06.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 36 3.4  
 AA505576, AA505576 nh93f03.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 36 3.4  
 H30276, H30276 yp42f05.s1 Homo sapiens cDNA clone 190113 3'. 36 3.4  
 AA699914, AA699914 zi61f08.s1 Soares fetal liver spleen 1NFLS... 36 3.4  
 AA595583, AA595583 nk92c04.s1 NCI\_CGAP\_Co11 Homo sapiens cDNA... 36 3.4  
 AA351139, AA351139 EST58769 Infant brain Homo sapiens cDNA 5'... 36 3.4  
 AA810167, AA810167 ob88a03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 36 3.4  
 H50257, H50257 yo28a07.r1 Homo sapiens cDNA clone 179220 5'. 36 3.4  
 W19939, W19939 zb37e09.r1 Soares parathyroid tumor NbHPA Homo... 36 3.4  
 R19840, R19840 yg30e11.r1 Homo sapiens cDNA clone 33837 5'. 36 3.4  
 AA514234, AA514234 nf56e10.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 36 3.4

AA183407, AA183407 ms  
 AA821640, AA821640 vw  
 AA289310, AA289310

AA900756, AA900756 UI-R-E0-di-d-04-0-UI.s1 UI-R-E0 Rattus nor... 46 0.001  
 T18416, T18416 6c02e07t7 etiolated seedling Zea mays cDNA clo... 40 0.069  
 AA817427, AA817427 LD22827.5prime LD Drosophila melanogaster ... 36 1.1  
 AA274351, AA274351 TgESTzz25c09.s1 TgME49 invivo Bradyzoite c... 36 1.1  
 AA391823, AA391823 LD10747.5prime LD Drosophila melanogaster ... 36 1.1  
 AA274275, AA274275 TgESTzz24b02.s1 TgME49 invivo Bradyzoite c... 34 4.3  
 R86490, R86490 RABEST068T Oryctolagus cuniculus cDNA clone pR... 34 4.3  
 AA965817, AA965817 o5g08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.3

SEQ ID NO:560

X81198, L35746, L49403, U21317, Z35640, AL010273, U09850, AF071771, Z96434,

Z50028, X72735, U13072, Z34294, AB002109, X68401, M92840, D88399, Z36238, AF000262, Z46828,

# HUMAN ESTs

AA215808, AA215808 zr98b10.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 1082 0.0  
 N75131, N75131 yz29g07.r1 Soares multiple sclerosis 2NbHMSP H... 989 0.0  
 AA709149, AA709149 zf98g05.s1 Soares fetal heart NbHH19W Homo... 985 0.0  
 AA428341, AA428341 zw18f09.s1 Soares ovary tumor NbHOT Homo s... 967 0.0  
 AA043426, AA043426 zk54h09.r1 Soares pregnant uterus NbHPU Ho... 870 0.0  
 AA878521, AA878521 oj19c01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 844 0.0  
 AA599696, AA599696 ag10h01.s1 Gessler Wilms tumor Homo sapien... 842 0.0  
 W52304, W52304 zc47c08.r1 Soares senescent fibroblasts NbHSF ... 841 0.0  
 AA043427, AA043427 zk54h09.s1 Soares pregnant uterus NbHPU Ho... 769 0.0  
 N64314, N64314 yz46a12.s1 Homo sapiens cDNA clone 286078 3'. 763 0.0  
 N52360, N52360 yz29g07.s1 Soares multiple sclerosis 2NbHMSP H... 753 0.0  
 AA290863, AA290863 zt19a08.s1 Soares ovary tumor NbHOT Homo s... 747 0.0  
 AA768023, AA768023 oa60e03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 728 0.0  
 AA872018, AA872018 oi05f08.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 718 0.0  
 AA164765, AA164765 zp01g09.s1 Stratagene ovarian cancer (#937... 716 0.0  
 AA814881, AA814881 oa75e02.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 708 0.0  
 R86915, R86915 yq30f07.r1 Homo sapiens cDNA clone 197317 5'. 692 0.0  
 W56703, W56703 zd14e01.r1 Soares fetal heart NbHH19W Homo sap... 642 0.0  
 R84872, R84872 yq27e01.r1 Soares fetal liver spleen 1NFLS Hom... 636 0.0  
 D79691, HUM307D10B Human aorta cDNA 5'-end GEN-307D10. 630 e-179  
 AA025638, AA025638 ze90d11.s1 Soares fetal heart NbHH19W Homo... 626 e-178  
 AA298883, AA298883 EST114512 Pancreas tumor I Homo sapiens cD... 624 e-177  
 R86903, R86903 yq30d07.r1 Homo sapiens cDNA clone 197293 5'. 622 e-176  
 AA033584, AA033584 zk21b12.s1 Soares pregnant uterus NbHPU Ho... 618 e-175  
 AA633335, AA633335 nq58h09.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 611 e-173  
 AA298894, AA298894 EST114513 Pancreas tumor I Homo sapiens cD... 599 e-169  
 R85806, R85806 yq27e01.s1 Soares fetal liver spleen 1NFLS Hom... 595 e-168  
 AA872617, AA872617 oi05g07.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 591 e-167  
 H71458, H71458 yu71a06.s1 Homo sapiens cDNA clone 239218 3'. 587 e-166  
 AA291045, AA291045 zt19a08.r1 Soares ovary tumor NbHOT Homo s... 563 e-159  
 H71587, H71587 yu71a06.r1 Homo sapiens cDNA clone 239218 5'. 543 e-153  
 AA035172, AA035172 zk28g05.s1 Soares pregnant uterus NbHPU Ho... 523 e-147  
 AA164764, AA164764 zp01g09.r1 Stratagene ovarian cancer (#937... 517 e-145  
 AA297001, AA297001 EST112550 Adipose tissue. white II Homo sa... 502 e-140  
 AA296816, AA296816 EST112381 Aorta endothelial cells Homo sap... 500 e-139  
 AA769090, AA769090 oa74e12.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 494 e-138  
 H54447, H54447 yq91f04.s1 Homo sapiens cDNA clone 203167 3'. 438 e-121  
 H54537, H54537 yq91f04.r1 Homo sapiens cDNA clone 203167 5'. 436 e-120  
 AI049757, AI049757 an26g03.x1 Gessler Wilms tumor Homo sapien... 430 e-119

AA033583, AA033583 zk21b12.r1 Soares pregnant uterus NbHPU Ho... 422 e-116  
D61748, HUM205G02B Human aorta cDNA 5'-end GEN-205G02. 412 e-113  
AA148635, AA148635 zl26d10.r1 Soares pregnant uterus NbHPU Ho... 377 e-102  
AA148636, AA148636 zl26d10.s1 Soares pregnant uterus NbHPU Ho... 373 e-101  
AA025637, AA025637 ze90d11.r1 Soares fetal heart NbHH19W Homo... 371 e-101  
AA932620, AA932620 oo61h04.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 365 4e-99  
AA385594, AA385594 EST99296 Thyroid Homo sapiens cDNA 5' end 339 2e-91  
AA361957, AA361957 EST71295 T-cell lymphoma Homo sapiens cDNA... 289 2e-76  
AA383998, AA383998 EST97483 Thyroid Homo sapiens cDNA 5' end ... 274 1e-71  
H22175, H22175 yl38a03.r1 Homo sapiens cDNA clone 160492 5'. 256 3e-66  
R50060, R50060 yj59c10.r1 Homo sapiens cDNA clone 153042 5'. 256 3e-66  
AA229414, AA229414 nc47f12.r1 NCI\_CGAP\_Pr3 Homo sapiens cDNA ... 246 3e-63  
D20466, HUMGS01440 Human HL60 3'directed MboI cDNA, HUMGS014... 208 6e-52  
AA249061, AA249061 ll4438.seq.F Human fetal heart, Lambda ZAP... 168 5e-40  
R86758, R86758 yq30f07.s1 Homo sapiens cDNA clone 197317 3'. 147 2e-33  
R58025, R58025 F8018 Fetal heart Homo sapiens cDNA clone F801... 101 1e-19  
AA371076, AA371076 EST82846 Prostate gland I Homo sapiens cDN... 42 0.081  
AA977111, AA977111 oq24c03.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 40 0.32  
AA608923, AA608923 af03b04.s1 Soares testis NHT Homo sapiens ... 38 1.3

gb|AA386999|AA386999 vc81b02.r1 Ko mouse embryo 11 5dpc Mus mus... 668 0.0  
gb|AA589082|AA589082 vk24a08.r1 Knowles Solter mouse blastocyst... 658 0.0  
gb|AA510881|AA510881 vh59c11.r1 Soares mouse mammary gland NbMM... 617 e-175  
gb|AA763574|AA763574 vp07e08.r1 Soares mouse mammary gland NbMM... 615 e-174  
gb|AA387423|AA387423 vc84b03.r1 Ko mouse embryo 11 5dpc Mus mus... 549 e-155  
gb|AA915333|AA915333 vz28f05.r1 Soares 2NbMT Mus musculus cDNA ... 543 e-153  
gb|AA816208|AA816208 vp43c10.r1 Barstead mouse irradiated colon... 444 e-123  
gb|AA190043|AA190043 mt91h08.r1 Soares mouse lymph node NbMLN M... 424 e-117  
gb|AA207393|AA207393 mv89c09.r1 GuayWoodford Beier mouse kidney... 394 e-108  
emb|Z31258|MMTEST693 M.musculus expressed sequence tag MTEST693 309 8e-83  
gb|AA930143|AA930143 vz52d11.s1 Soares 2NbMT Mus musculus cDNA ... 293 5e-78  
gb|AA170612|AA170612 ms92c09.r1 Soares mouse 3NbMS Mus musculus... 287 3e-76  
gb|AA762238|AA762238 vw58h02.r1 Soares mouse mammary gland NMLM... 266 1e-69  
gb|AA689028|AA689028 vs02c12.r1 Barstead mouse irradiated colon... 264 4e-69  
gb|AA959938|AA959938 vw58h02.s1 Soares mouse mammary gland NMLM... 240 6e-62  
dbj|D18511|MUSGS01569 Mouse 3'-directed cDNA, MUSGS01569, clon... 172 1e-41  
gb|AA474393|AA474393 vd57g07.r1 Knowles Solter mouse blastocyst... 100 1e-19  
gb|W97165|W97165 mf90g05.r1 Soares mouse embryo NbME13.5 14.5 M... 74 8e-12  
gb|AA512077|AA512077 vj43f05.r1 Stratagene mouse skin (#937313)... 62 3e-08  
gb|AA794521|AA794521 vu68e07.r1 Stratagene mouse skin (#937313)... 54 8e-06  
gb|AA155454|AA155454 mn38h12.r1 Beddington mouse embryonic regi... 48 5e-04  
gb|W91000|W91000 mf83f06.r1 Soares mouse embryo NbMF13.5 14.5 M... 40 0.12

gb|AA219917|AA219917 mv62f05.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.45  
 gb|AA529349|AA529349 vi35f08.r1 Beddington mouse embryonic regi... 36 1.8  
 gb|AA754855|AA754855 vu51e08.r1 Soares mouse mammary gland NbMM... 36 1.8

gb|AA850379|AA850379 EST193146 Normalized rat ovary, Bento Soar... 569 e-161  
 gb|W63375|W63375 TgESTzy68g02.r1 TgME49 Tachyzoite cDNA Toxopla... 394 e-108  
 gb|AA946379|AA946379 EST201878 Normalized rat lung, Bento Soare... 353 5e-96  
 gb|AA964427|AA964427 UI-R-E1-gp-a-08-0-UI.s1 UI-R-E1 Rattus nor... 335 1e-90  
 gb|AA849599|AA849599 EST192366 Normalized rat muscle, Bento Soa... 307 3e-82  
 gb|AA849595|AA849595 EST192362 Normalized rat muscle, Bento Soa... 307 3e-82  
 gb|AA850378|AA850378 EST193145 Normalized rat ovary, Bento Soar... 278 3e-73  
 gb|AA957389|AA957389 UI-R-E1-fu-b-04-0-UI.s1 UI-R-E1 Rattus nor... 157 6e-37  
 gb|AI012981|AI012981 EST207432 Normalized rat spleen, Bento Soa... 147 6e-34  
 dbj|C48357|C48357 C.elegans cDNA clone yk469b2 : 5' end, single... 40 0.10  
 gb|AA440444|AA440444 LD15290.5prime LD Drosophila melanogaster ... 36 1.6  
 dbj|C22690|C22690 Rice cDNA, partial sequence (S5274\_4A) 36 1.6  
 gb|AA697626|AA697626 HL02895.5prime HL Drosophila melanogaster ... 36 1.6  
 gb|AA550136|AA550136 1244m3 gmbPfHB3.1. G. Roman Reddy Plasmodi... 36 1.6  
 gb|T43579|T43579 6842 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.6  
 gb|AI030501|AI030501 UI-R-C0-jc-g-02-0-UI.s1 UI-R-C0 Rattus nor... 36 1.6  
 gb|AA056876|AA056876 SWMFCA987SK Brugia malayi microfilaria cDN... 36 1.6  
 gb|AA440689|AA440689 LD15550.5prime LD Drosophila melanogaster ... 36 1.6

SEQ ID NO:561

emb|Z47552|HSFMO3 H.sapiens mRNA for flavin-containing monooxyg... 44 0.10  
 gb|U39966|HSFMO3G7 Homo sapiens flavin containing monooxygenase... 44 0.10  
 emb|AL021026|HS127D3 Homo sapiens DNA sequence from PAC 127D3 o... 44 0.10  
 gb|U35007|CPU35007 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10  
 gb|U35008|CPU35008 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10  
 dbj|D85068|RICT3A Rice transposable element T3 gene and ret... 42 0.40  
 dbj|D63711|RICT3 Rice transposon T3 DNA, complete sequence 42 0.40  
 gb|U01657|U01657 Carcharhinus plumbeus Ig lambda-chain gene, co... 42 0.40  
 emb|Z92540|HS179I15A Human DNA sequence from PAC 179I15, BRCA2 ... 40 1.6  
 dbj|AB001569|AB001569 Carrot DNA for transposon Tdc1 40 1.6  
 gb|AE000613|HPAE000613 Helicobacter pylori section 91 of 134 of... 40 1.6  
 emb|X07985|DMCUT Drosophila cut locus mRNA for homeodomain-cont... 40 1.6  
 gb|AC005217|AC005217 Homo sapiens chromosome 5, P1 clone 1047D6... 40 1.6

HUMAN ESTs

gb|AA401219|AA401219 zv63a03.r1 Soares total fetus Nb2HF8 9w Ho... 993 0.0  
 gb|H69371|H69371 yu19h09.r1 Homo sapiens cDNA clone 234305 5' s... 44 0.049  
 gb|N62576|N62576 za13d10.s1 Homo sapiens cDNA clone 292435 3' s... 42 0.19  
 gb|W77763|W77763 zd69c06.r1 Soares fetal heart NbHH19W Homo sap... 40 0.77  
 gb|R14832|R14832 yf93g05.r1 Homo sapiens cDNA clone 30203 5'. 40 0.77  
 gb|T90524|T90524 yd40a04.s1 Homo sapiens cDNA clone 110670 3' s... 38 3.0  
 gb|R91887|R91887 yq04c09.r1 Homo sapiens cDNA clone 195952 5'. 38 3.0  
 gb|AA586935|AA586935 nn68h03.s1 NCI\_CGAP\_Lar1 Homo sapiens cDNA... 38 3.0  
 gb|T46987|T46987 yb12a07.s1 Homo sapiens cDNA clone 70932 3' co... 38 3.0  
 gb|AA853975|AA853975 aj51f09.s1 Soares testis NHT Homo sapiens ... 38 3.0  
 gb|T97059|T97059 ye50e01.r1 Homo sapiens cDNA clone 121176 5'. 38 3.0  
 gb|AA883119|AA883119 am15h02.s1 Soares NFL T GBC S1 Homo sapien... 38 3.0  
 gb|AA860074|AA860074 ak45b06.s1 Soares testis NHT Homo sapiens ... 38 3.0  
 gb|AA889618|AA889618 ak28f06.s1 Soares\_testis\_NHT Homo sapiens ... 38 3.0

gb|AA230450|AA230450 mv73c06.r1 Soares mouse 3NME12 5 Mus muscu... 38 1.1  
 gb|AA058041|AA058041 mj58e08.r1 Soares mouse embryo NbME13.5 14... 38 1.1  
 gb|AA152953|AA152953 mq54a03.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1  
 gb|W34414|W34414 ma98b07.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.1  
 gb|AA465969|AA465969 ve90c06.s1 Knowles Solter mouse 2 cell Mus... 38 1.1  
 gb|AA261173|AA261173 mz62b11.r1 Soares mouse lymph node NbMLN M... 38 1.1  
 gb|AA238109|AA238109 mw97b05.r1 Soares mouse NML Mus musculus c... 38 1.1  
 dbj|C86549|C86549 Mus musculus fertilized egg cDNA 3'-end seque... 38 1.1  
 gb|AI048677|AI048677 ub29g09.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1  
 dbj|D77921|MUSC1A08 Mouse embryonal carcinoma F9 cell cDNA, C1A08 38 1.1  
 gb|AA396183|AA396183 vb45e04.r1 Soares mouse lymph node NbMLN M... 38 1.1  
 gb|AA465898|AA465898 vc62f12.s1 Knowles Solter mouse 2 cell Mus... 36 4.3  
 gb|AA041869|AA041869 mj05b12.r1 Soares mouse embryo NbME13.5 14... 36 4.3  
 gb|AA637824|AA637824 vr21f11.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3  
 gb|W82563|W82563 mf05g06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.3  
 gb|AA389972|AA389972 vb30e03.r1 Soares mouse lymph node NbMLN M... 36 4.3  
 gb|AA396253|AA396253 vb45f08.r1 Soares mouse lymph node NbMLN M... 36 4.3  
 gb|AA920907|AA920907 vy84f04.r1 Stratagene mouse macrophage (#9... 36 4.3  
 gb|AA517166|AA517166 vh98h05.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3  
 gb|AA433599|AA433599 vf47a05.r1 Soares mouse NbMH Mus musculus ... 36 4.3  
 gb|AA867252|AA867252 vx25c01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.3  
 dbj|C85619|C85619 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.3  
 gb|AA260277|AA260277 va93g05.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.3  
 gb|AA172548|AA172548 mt04g11.r1 Soares mouse 3NbMS Mus musculus... 36 4.3  
 gb|AA266879|AA266879 mz96a02.r1 Soares mouse lymph node NbMLN M... 36 4.3  
 gb|AA473019|AA473019 vd43e06.r1 Barstead MPLRB1 Mus musculus cD... 36 4.3

gb|R47549|R47549 SW3ICA119SK *Brugia malayi* infective larva cDNA... 40 0.24  
 gb|H32651|H32651 EST107947 Rat PC-12 cells, untreated *Rattus* sp... 38 0.96  
 gb|AA955987|AA955987 UI-R-E1-fb-f-06-0-UI.s1 UI-R-E1 *Rattus* nor... 38 0.96  
 gb|AA819638|AA819638 UI-R-A0-an-f-03-0-UI.s1 UI-R-A0 *Rattus* nor... 38 0.96  
 gb|AI010914|AI010914 EST205365 Normalized rat muscle, Bento Soa... 38 0.96  
 gb|AA893199|AA893199 EST197002 Normalized rat kidney, Bento Soa... 38 0.96  
 gb|AA945176|AA945176 EST200675 Normalized rat liver, Bento Soar... 38 0.96  
 gb|R95272|R95272 SWOvL3CA167SK *Onchocerca volvulus* infective la... 36 3.8  
 gb|AA917208|AA917208 ka05f02.s1 *Onchocerca volvulus* infective l... 36 3.8  
 dbj|C62023|C62023 *C.elegans* cDNA clone yk249d5 : 5' end, single... 36 3.8  
 gb|AI013322|AI013322 EST207997 Normalized rat spleen, Bento Soa... 36 3.8  
 gb|AI043280|AI043280 TENU0920 *T. cruzi* epimastigote normalized ... 36 3.8  
 gb|AI009422|AI009422 EST203873 Normalized rat heart, Bento Soar... 36 3.8  
 gb|AI012655|AI012655 EST207106 Normalized rat placenta, Bento S... 36 3.8  
 dbj|C62878|C62878 *C.elegans* cDNA clone yk296d4 : 5' end, single... 36 3.8  
 gb|AA915818|AA915818 SWOvL3CA1269SK *Onchocerca volvulus* infecti... 36 3.8  
 gb|W00009|W00009 TgESTzy75b07.r1 TgRH Tachyzoite cDNA *Toxoplasma*... 36 3.8  
 gb|AA943503|AA943503 EST199002 Normalized rat brain, Bento Soar... 36 3.8  
 gb|AA956933|AA956933 UI-R-E1-fl-b-08-0-UI.s1 UI-R-E1 *Rattus* nor... 36 3.8  
 gb|H54977|H54977 HHU16a *Sorghum bicolor* cv. TX430 *Sorghum bicol*... 36 3.8

SEQ ID NO:562

gb|AC000112|HSAC000112 Human PAC clone DJ149P21, complete seque... 44 0.082  
 gb|U50197|CELF25E2 *Caenorhabditis elegans* cosmid F25E2. 44 0.082  
 dbj|AB007727|AB007727 *Arabidopsis thaliana* genomic DNA. chromos... 44 0.082  
 gb|U02562|BSU02562 *Bacillus subtilis* N-acetylglucosaminidase (l... 42 0.32  
 dbj|D45048|BACORFX *Bacillus subtilis* gene for beta-N-acetylgluc... 42 0.32  
 emb|Z70683|CEF13B12 *Caenorhabditis elegans* cosmid F13B12, compl... 40 1.3  
 emb|AL023828|CEY17G7B *Caenorhabditis elegans* cosmid Y17G7B, com... 40 1.3  
 gb|U39740|CELZC64 *Caenorhabditis elegans* cosmid ZC64. 40 1.3  
 gb|AF006490|AF006490 *Gossypium hirsutum* adenine nucleotide tran... 40 1.3  
 emb|AL010170|PFSC03098 *Plasmodium falciparum* DNA \*\*\* SEQUENCING... 40 1.3  
 gb|U53701|GHU53701 *Gossypium hirsutum* alcohol dehydrogenase 2d ... 40 1.3

#### HUMAN ESTs

gb|AA670455|AA670455 ae62h05.s1 Stratagene lung carcinoma 93721... 852 0.0  
 gb|AA251062|AA251062 zs07c10.r1 NCI\_CGAP GCBI Homo sapiens cDNA... 795 0.0

gb|AA669916|AA669916 ag42h08.s1 Jia bone marrow stroma Homo sap... 638 0.0  
 gb|AA300058|AA300058 EST12665 Uterus tumor I Homo sapiens cDNA ... 587 e-165  
 gb|AA664277|AA664277 ac08c05.s1 Stratagene HeLa cell s3 937216 ... 549 e-154  
 gb|AA373224|AA373224 EST85230 HSC172 cells I Homo sapiens cDNA ... 529 e-148  
 gb|AA225705|AA225705 nc10b05.r1 NCI\_CGAP\_Pr1 Homo sapiens cDNA ... 515 e-144  
 gb|W27883|W27883 39b10 Human retina cDNA randomly primed sublib... 484 e-134  
 gb|R24643|R24643 yh36g05.r1 Homo sapiens cDNA clone 131864 5'. 438 e-121  
 gb|N93137|N93137 zb28h06.s1 Homo sapiens cDNA clone 304955 3'. 432 e-119  
 gb|AA250933|AA250933 zs07d01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 426 e-117  
 gb|AA216370|AA216370 nc10b05.s1 NCI\_CGAP\_Pr1 Homo sapiens cDNA ... 398 e-109  
 gb|H26939|H26939 yl64g01.r1 Homo sapiens cDNA clone 163056 5'. 394 e-108  
 gb|H30169|H30169 yo58g09.r1 Homo sapiens cDNA clone 182176 5'. 394 e-108  
 gb|W38854|W38854 zb28h06.r1 Soares parathyroid tumor NbHPA Homo... 359 5e-97  
 gb|AA602297|AA602297 np25a11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 281 1e-73  
 gb|AA167151|AA167151 zp06e09.r1 Stratagene ovarian cancer (#937... 256 6e-66  
 gb|AA172387|AA172387 zo99d03.s1 Stratagene ovarian cancer (#937... 234 2e-59  
 gb|AA173748|AA173748 zo99d03.r1 Stratagene ovarian cancer (#937... 224 2e-56  
 gb|T83979|T83979 yd66a11.s1 Homo sapiens cDNA clone 113180 3'. 220 3e-55  
 dbj|D61540|HUM415A08B Human fetal brain cDNA 5'-end GEN-415A08. 194 2e-47  
 gb|N45148|N45148 yv25a05.r1 Homo sapiens cDNA clone 243728 5'. 165 2e-38  
 gb|AA642960|AA642960 60f07.s1 NCI\_CGAP\_Lym3 Homo sapiens cDNA... 147 4e-33  
 gb|R90980|R90980 yp93a03.r1 Homo sapiens cDNA clone 194956 5' s... 40 0.62  
 gb|AA521500|AA521500 aa73h08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.62  
 gb|H82921|H82921 yq46h10.s1 Homo sapiens cDNA clone 198883 3' s... 40 0.62  
 gb|AA294871|AA294871 EST100023 Pancreas tumor I Homo sapiens cD... 38 2.4  
 dbj|D63191|HUM503F11B Human placenta cDNA 5'-end GEN-503F11. 38 2.4  
 gb|AA211096|AA211096 zq89g01.s1 Stratagene hNT neuron (#937233)... 38 2.4

gb|AA840137|AA840137 ud01e08.r1 Soares mouse uterus NMPu Mus mu... 383 e-104  
 gb|AA145994|AA145994 mr13h04.r1 Soares mouse 3NbMS Mus musculus... 345 3e-93  
 gb|AA146365|AA146365 mr05d05.r1 Soares mouse 3NbMS Mus musculus... 236 2e-60  
 gb|AA203902|AA203902 mu60f02.r1 Soares mouse lymph node NbMLN M... 236 2e-60  
 gb|AA204516|AA204516 mu66c10.r1 Soares mouse lymph node NbMLN M... 182 2e-44  
 gb|AA137343|AA137343 mq80g08.r1 Stratagene mouse melanoma (#937... 52 6e-05  
 gb|AA174717|AA174717 ms67a01.r1 Soares mouse 3NbMS Mus musculus... 48 0.001  
 gb|W34073|W34073 ma85d10.r1 Soares mouse p3NMF19.5 Mus musculus... 48 0.001  
 gb|AA289493|AA289493 vb36b01.r1 Soares mouse lymph node NbMLN M... 48 0.001  
 gb|AA177700|AA177700 mt33e12.r1 Soares mouse 3NbMS Mus musculus... 48 0.001  
 gb|AA146021|AA146021 mr13e03.r1 Soares mouse 3NbMS Mus musculus... 48 0.001  
 gb|AA155352|AA155352 mn43d09.r1 Beddington mouse embryonic regi... 46 0.004  
 gb|AA880874|AA880874 vx33b02.r1 Stratagene mouse lung 937302 Mu... 42 0.056



gb|AA590520|AA590520 vi54b08.r1 Beddington mouse embryonic regi... 38 0.88  
gb|AA596629|AA596629 vm56e06.r1 Stratagene mouse Tcell 937311 M... 38 0.88  
dbj|D76657|MUS75H09 Mouse embryonal carcinoma F9 cell cDNA, 75H09 38 0.88  
gb|AA050336|AA050336 mj12f05.r1 Soares mouse embryo NbME13.5 14... 38 0.88  
gb|AA120196|AA120196 mn35a12.r1 Beddington mouse embryonic regi... 38 0.88  
gb|W85267|W85267 mf42c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5  
gb|AA239372|AA239372 my38f03.r1 Barstead mouse pooled organs MP... 36 3.5  
gb|AA497891|AA497891 vi73c07.r1 Stratagene mouse testis (#93730... 36 3.5  
gb|AA673053|AA673053 vn45e05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.5  
emb|Z36324|MM224 M.musculus mRNA (clone 224) for expressed sequ... 36 3.5  
gb|AI021128|AI021128 ub01f06.r1 Soares mouse mammary gland NbMM... 36 3.5  
gb|AA403424|AA403424 mz56f07.r1 Barstead mouse pooled organs MP... 36 3.5  
gb|W66683|W66683 me23g11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5  
gb|AA689022|AA689022 vs02c03.r1 Barstead mouse irradiated colon... 36 3.5  
gb|AA574590|AA574590 vn63h11.r1 Barstead mouse proximal colon M... 36 3.5

dbj|C90696|C90696 Dictyostelium discoideum slug cDNA, clone SSJ634 38 0.78  
gb|AA269052|AA269052 MA1MA052.AA3 S. mansoni adult Lambda Zap S... 38 0.78  
gb|AA998786|AA998786 UI-R-C0-im-e-11-0-UI.s1 UI-R-C0 Rattus nor... 38 0.78  
gb|H33464|H33464 EST109494 Rat PC-12 cells. NGF-treated (9 days... 38 0.78  
gb|AA390721|AA390721 LD09459.5prime LD Drosophila melanogaster ... 36 3.1  
dbj|C83908|C83908 Dictyostelium discoideum slug cDNA, clone SSA567 36 3.1  
gb|AA202425|AA202425 LD02606.5prime LD Drosophila melanogaster ... 36 3.1  
gb|AI030951|AI030951 UI-R-C0-jf-d-04-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1  
gb|N60251|N60251 TgESTzy11d04.r1 TgRH Tachyzoite cDNA Toxoplasma... 36 3.1  
gb|AA246875|AA246875 LD05855.5prime LD Drosophila melanogaster ... 36 3.1  
gb|AA803682|AA803682 GM13955.5prime GM Drosophila melanogaster ... 36 3.1  
gb|AA997528|AA997528 UI-R-C0-hw-h-11-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1  
gb|AA695197|AA695197 GM02389.5prime GM Drosophila melanogaster ... 36 3.1  
gb|AA567339|AA567339 HL01077.5prime HL Drosophila melanogaster ... 36 3.1  
gb|AA950648|AA950648 LD30547.5prime LD Drosophila melanogaster ... 36 3.1

SEQ ID NO:563

substantially identical to D86956

SEQ ID NO:564

gb|AC004505|AC004505 Homo sapiens chromosome 20, P1 clone 86C1 ... 176 1e-41  
 gb|S78798|S78798 1-phosphatidylinositol-4-phosphate 5-kinase is... 115 4e-23  
 gb|U48696|HSU48696 Human mariner-like element-containing mRNA, ... 115 4e-23  
 gb|U66300|LEU66300 Lycopersicon esculentum heat shock protein (... 115 4e-23  
 gb|AF045432|AF045432 Danio rerio stem cell leukemia protein (ta... 111 6e-22  
 emb|Z97178|BVRNAEF2 Beta vulgaris cDNA for elongation factor 2 107 9e-21  
 gb|U39066|MMU39066 Murine MAP kinase kinase 6c mRNA, complete cds. 101 6e-19  
 gb|U37573|XXU37573 Shuttle expression vector pBKCMV. 96 4e-17  
 gb|AF033097|AF033097 Avena sativa nonphototropic hypocotyl 1 (N... 90 2e-15  
 gb|AF027174|AF027174 Arabidopsis thaliana cellulose synthase ca... 86 3e-14  
 gb|U65376|CFU65376 Canis familiaris rod photoreceptor transduci... 84 1e-13  
 gb|AF033565|AF033565 Mus musculus cdc2/CDC28-like protein kinas... 82 5e-13  
 emb|Z49980|HS2AMCP H.sapiens mRNA for ets-like protein (clone 7... 82 5e-13  
 emb|AJ001103|LLARCAB Lactococcus lactis arcA and arcB genes 80 2e-12  
 gb|U52868|CFU52868 Canis familiaris retinal cyclic-GMP phosphod... 80 2e-12  
 gb|G29058|G29058 chicken STS ADL368 76 3e-11  
 gb|G29060|G29060 chicken STS ADL352 76 3e-11  
 gb|U34048|HDU34048 Haemophilus ducreyi hemoglobin-binding prote... 76 3e-11  
 gb|U44386|SLU44386 Solanum lycopersicum heat shock protein (TFH... 68 8e-09  
 gb|S83098|S83098 ribosomal protein S3 [Ambystoma mexicanum=Mexi... 66 3e-08  
 gb|U48697|HSU48697 Human mariner-like element-containing mRNA, ... 60 2e-06  
 gb|AF033096|AF033096 Avena sativa nonphototropic hypocotyl 1 (N... 60 2e-06  
 emb|X99051|LLATTMSAT L.lagopus ATT microsatellite, locus LLST1 58 8e-06  
 gb|U41811|HAU41811 Homarus americanus beta-I tubulin mRNA, comp... 46 0.029  
 emb|X99055|LLCAMSAT1 L.lagopus CA microsatellite, locus LLSD5 44 0.12  
 emb|X65215|BTMISATN B.taurus microsatellite DNA (624bp) 44 0.12  
 gb|AE001023|AE001023 Archaeoglobus fulgidus section 84 of 172 o... 42 0.46  
 emb|X80164|HSPDCM4 H.salinarium phage dcm4 Virus DNA 42 0.46  
 emb|X87859|MTCMAJ12S C.major mitochondrial gene for 12S ribosom... 42 0.46  
 emb|X87861|MTCPAL12S C.pallidus mitochondrial gene for 12S ribo... 42 0.46  
 gb|L13767|STMSEC101A Streptomyces lividans sec101 gene, 5' end p... 42 0.46  
 emb|Y08962|OSTRAMBPR O.sativa mRNA for transmembrane protein >g... 40 1.8  
 gb|S65686|S65686 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 gb|J02871|HUMCP45IV Human lung cytochrome P450 (IV subfamily) B... 40 1.8  
 dbj|D10450|HUMRTVE Human genomic DNA, retrovirus-like element 40 1.8  
 gb|S65683|S65683 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 gb|L14950|PIGALDRED Sus scrofa aldose reductase mRNA, complete ... 40 1.8  
 gb|S65693|S65693 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 gb|S65694|S65694 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 emb|AJ223292|SPAJ3292 Streptococcus pyogenes SOD gene, complete... 40 1.8  
 gb|U25846|HAU25846 Homarus americanus clone LOB5 farnesoic acid... 40 1.8  
 emb|X16699|HSP450P2 Human mRNA for cytochrome P-450HP 40 1.8  
 gb|U37100|HSU37100 Homo sapiens aldose reductase-like peptide m... 40 1.8

## HUMAN ESTs

gb|AA305996|AA305996 EST177003 Jurkat T-cells VI Homo sapiens c... 942 0.0  
 gb|AA975279|AA975279 oq36e08.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 900 0.0  
 gb|AA426359|AA426359 zw11b02.r1 Soares NhHMPu S1 Homo sapiens c... 868 0.0  
 gb|AA424296|AA424296 zv90b08.r1 Soares NhHMPu S1 Homo sapiens c... 749 0.0  
 gb|AA632259|AA632259 np67d04.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 730 0.0  
 gb|H80377|H80377 yu59e01.r1 Homo sapiens cDNA clone 230424 5'. 658 0.0  
 gb|AA515175|AA515175 ng68f10.s1 NCI\_CGAP\_Lip2 Homo sapiens cDNA... 615 e-174  
 gb|AA351770|AA351770 EST59616 Infant brain Homo sapiens cDNA 5'... 611 e-172  
 gb|AA426522|AA426522 zw11b02.s1 Soares NhHMPu S1 Homo sapiens c... 587 e-165  
 gb|AA676220|AA676220 zi22a12.s1 Soares fetal liver spleen 1NFLS... 585 e-165  
 gb|R35132|R35132 yg60e09.r1 Homo sapiens cDNA clone 36874 5'. 579 e-163  
 gb|H80280|H80280 yu59e01.s1 Homo sapiens cDNA clone 230424 3'. 579 e-163  
 gb|H81145|H81145 yu60e01.r1 Homo sapiens cDNA clone 230520 5'. 561 e-157  
 gb|AA311105|AA311105 EST18187 Heart I Homo sapiens cDNA 5' end 533 e-149  
 gb|AA380530|AA380530 EST93691 Supt cells Homo sapiens cDNA 5' end 527 e-147  
 gb|H81050|H81050 yu60e01.s1 Homo sapiens cDNA clone 230520 3'. 500 e-139  
 gb|AA460005|AA460005 zx49g07.s1 Soares testis NHT Homo sapiens ... 482 e-134  
 gb|AA076450|AA076450 zm91d12.r1 Stratagene ovarian cancer (#937... 466 e-129  
 gb|N43873|N43873 yy43e09.r1 Homo sapiens cDNA clone 274024 5'. 452 e-125  
 gb|AA076451|AA076451 zm91d12.s1 Stratagene ovarian cancer (#937... 418 e-115  
 gb|AA907095|AA907095 ol03b12.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 414 e-113  
 gb|W01027|W01027 za56g07.r1 Soares fetal liver spleen 1NFLS Hom... 262 1e-67  
 gb|AA127183|AA127183 zn29d11.r1 Stratagene neuroepithelium NT2R... 222 1e-55  
 gb|H65491|H65491 yr56a08.s1 Homo sapiens cDNA clone 209270 3'. 222 1e-55  
 gb|N48543|N48543 yy49d08.r1 Homo sapiens cDNA clone 276879 5'. 210 4e-52  
 gb|R32579|R32579 yh54h06.r1 Homo sapiens cDNA clone 133595 5'. 194 2e-47  
 gb|AA247827|AA247827 j0778.seq.F Human fetal heart, Lambda ZAP ... 117 5e-24  
 N84048, (many others similar, but smaller)

gb|AA589598|AA589598 vl49d08.s1 Stratagene mouse skin (#937313)... 398 e-109  
 gb|AA647465|AA647465 vq82f02.s1 Knowles Solter mouse 2 cell Mus... 385 e-105  
 gb|AA510284|AA510284 vh58f02.r1 Soares mouse mammary gland NbMM... 345 4e-93  
 gb|AA028696|AA028696 ml12e12.r1 Soares mouse p3NMF19.5 Mus musc... 307 9e-82  
 gb|N28081|N28081 MDB1409R Mouse brain, Stratagene Mus musculus ... 244 1e-62  
 gb|AA177452|AA177452 mt24c12.r1 Soares mouse 3NbMS Mus musculus... 226 3e-57  
 gb|N28080|N28080 MDB1409 Mouse brain, Stratagene Mus musculus c... 226 3e-57  
 dbj|C88310|C88310 Mus musculus fertilized egg cDNA 3'-end seque... 226 3e-57  
 gb|AA763786|AA763786 vo99g12.r1 Soares mouse mammary gland NbMM... 94 2e-17  
 gb|AA667535|AA667535 vv18b12.r1 Stratagene mouse heart (#937316... 40 0.31  
 gb|AA208274|AA208274 mv96a01.r1 GuayWoodford Beier mouse kidney... 38 1.2

gb|AA444814|AA444814 vg50e04.r1 Soares mouse mammary gland NbMM... 38 1.2  
 gb|AA763341|AA763341 vw53b12.r1 Soares mouse mammary gland NMLM... 38 1.2  
 gb|AA110827|AA110827 mp57a12.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2  
 gb|AA691932|AA691932 vt06b04.r1 Barstead mouse myotubes MPLRB5 ... 38 1.2  
 gb|W77233|W77233 me61f11.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2  
 gb|AA072872|AA072872 mm80g08.r1 Stratagene mouse embryonic carc... 38 1.2  
 gb|AA980630|AA980630 ua43f05.r1 Soares mouse mammary gland NbMM... 36 4.9  
 gb|AA065522|AA065522 ml54d09.r1 Stratagene mouse testis (#93730... 36 4.9  
 gb|AA982398|AA982398 uh07b08.r1 Soares mouse hypothalamus NMHy ... 36 4.9  
 gb|W62610|W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9  
 gb|AA286651|AA286651 vb79b02.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.9  
 gb|AA399772|AA399772 vd70g05.r1 Beddington mouse embryonic regi... 36 4.9  
 gb|AA510475|AA510475 vg32h08.r1 Soares mouse mammary gland NbMM... 36 4.9  
 gb|AA109064|AA109064 ml63g02.r1 Stratagene mouse testis (#93730... 36 4.9  
 gb|AA033485|AA033485 mi42c08.r1 Soares mouse embryo NbME13.5 14... 36 4.9  
 gb|W57221|W57221 md59g10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9  
 gb|AA467106|AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 36 4.9  
 gb|W97470|W97470 mf95a11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9  
 gb|AA606917|AA606917 vm91c05.r1 Knowles Solter mouse blastocyst... 36 4.9  
 dbj|C78330|C78330 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9  
 gb|AA013753|AA013753 mh26h12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9  
 gb|AA145240|AA145240 mr12a03.r1 Soares mouse 3NbMS Mus musculus... 36 4.9  
 gb|AA245533|AA245533 mx03c11.r1 Soares mouse NML Mus musculus c... 36 4.9  
 gb|AA770893|AA770893 vt13a08.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9  
 dbj|C79987|C79987 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9  
 gb|AA014027|AA014027 mh24a12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9  
 dbj|C89051|C89051 Mus musculus early blastocyst cDNA, clone 01B... 36 4.9  
 gb|AA058308|AA058308 mj59e09.r1 Soares mouse embryo NbME13.5 14... 36 4.9  
 gb|AA673826|AA673826 vu08h10.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9  
 gb|AA637080|AA637080 vn07h04.r1 Knowles Solter mouse blastocyst... 36 4.9  
 gb|W44292|W44292 mc80c07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9

gb|AA955972|AA955972 UI-R-E1-ff-d-10-0-UI.s1 UI-R-E1 Rattus nor... 159 4e-37  
 gb|AA957275|AA957275 UI-R-E1-fq-f-08-0-UI.s1 UI-R-E1 Rattus nor... 157 2e-36  
 emb|Z84031|SSZ84031 S.scrofa mRNA; expressed sequence tag (5'; ... 111 9e-23  
 gb|AF041408|AF041408 Fragaria x ananassa clone FA110b 96 5e-18  
 gb|AA933116|AA933116 SWBmL3SA048T3 Brugia malayi L3 subtracted ... 58 1e-06  
 gb|AA933363|AA933363 SWBmL3SA615T3 Brugia malayi L3 subtracted ... 52 7e-05  
 gb|AA660164|AA660164 00001 MtrHE Medicago truncatula cDNA 5' si... 50 3e-04  
 gb|N37420|N37420 18647 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018  
 gb|H35981|H35981 14503 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018  
 gb|AA882627|AA882627 TENS0198 T. cruzi epimastigote normalized ... 44 0.018  
 gb|AI026481|AI026481 TENU0693 T. cruzi epimastigote normalized ... 42 0.070  
 gb|AA946369|AA946369 EST201868 Normalized rat lung. Bento Soare... 42 0.070

gb|AI010371|AI010371 EST204822 Normalized rat lung, Bento Soare... 42 0.070  
 gb|AI010257|AI010257 EST204708 Normalized rat lung, Bento Soare... 42 0.070  
 dbj|D39318|RICR3325A Rice cDNA, partial sequence (R3325\_1A). 40 0.28  
 gb|U40140|OSU40140 Oryza sativa clone pFDRRC22 mRNA sequence. 40 0.28  
 gb|AI009132|AI009132 EST203583 Normalized rat embryo, Bento Soa... 40 0.28  
 dbj|D47291|RICS12574A Rice cDNA, partial sequence (S12574\_1A). 40 0.28  
 dbj|D47316|RICS12613A Rice cDNA, partial sequence (S12613\_1A). 40 0.28  
 gb|T42265|T42265 5528 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 40 0.28  
 dbj|D47631|RICS13239A Rice cDNA, partial sequence (S13239\_1A). 40 0.28  
 gb|AI013513|AI013513 EST208188 Normalized rat spleen, Bento Soa... 40 0.28  
 gb|AA751980|AA751980 96AS0896 Rice Immature Seed Lambda ZAPII c... 40 0.28  
 gb|AA660165|AA660165 00002 MtRHE Medicago truncatula cDNA 5' si... 40 0.28  
 emb|Z34868|ATTS3597 A. thaliana transcribed sequence; clone FAF... 40 0.28  
 dbj|D39131|RICR2302A Rice cDNA, partial sequence (R2302\_1A). 40 0.28  
 gb|AA963968|AA963968 UI-R-C0-gs-b-05-0-UI.s1 UI-R-C0 Rattus nor... 40 0.28  
 gb|AA866346|AA866346 UI-R-A0-bm-a-05-0-UI.s1 UI-R-A0 Rattus nor... 40 0.28  
 gb|AI044437|AI044437 UI-R-C1-js-e-06-0-UI.s1 UI-R-C1 Rattus nor... 40 0.28  
 dbj|D41811|RICS4634A Rice cDNA, partial sequence (S4634\_1A). 40 0.28  
 dbj|C19261|C19261 Rice cDNA, partial sequence (E10176\_1A) 40 0.28  
 dbj|D48409|RICS14588A Rice cDNA, partial sequence (S14588\_1A). 40 0.28  
 dbj|C26556|C26556 Rice cDNA, partial sequence (C12586\_1A) 40 0.28  
 dbj|D47831|RICS13548A Rice cDNA, partial sequence (S13548\_1A). 40 0.28  
 dbj|C72152|C72152 Rice cDNA, partial sequence (E1094\_3A) 40 0.28  
 dbj|D46553|RICS11305A Rice cDNA, partial sequence (S11305\_2A). 40 0.28  
 gb|AI028926|AI0289 (and many others of similar score)

SEQ ID NO:565

emb|X68308|OOLPLIP O.ovis mRNA for lipoprotein lipase 40 1.2  
 gb|AE000660|HUA000660 Homo sapiens T-cell receptor alpha delta... 40 1.2  
 emb|AL022333|HS474I12 Human DNA sequence \*\*\* SEQUENCING IN PROG... 38 4.6  
 emb|Z12618|CFTRG C.fasciculata gene encoding trypanothione redu... 38 4.6  
 gb|M81651|HUMSEMIIB Human semenogelin II (SEMGII) gene, complet... 38 4.6  
 gb|M96980|HUMMYT1A Homo sapiens myelin transcription factor 1 (... 38 4.6  
 gb|U89688|ACU89688 Acanthamoeba castellanii myosin-I binding pr... 38 4.6  
 gb|AC002497|AC002497 Human Cosmid g1940a142 from 7q31.3, comple... 38 4.6  
 gb|M81652|HUMSMNGLN Homo sapiens semenogelin II mRNA, complete ... 38 4.6  
 gb|M25665|HUMNCF1A Human neutrophil cytosol factor 1 (NCF-47k) ... 38 4.6  
 gb|M73325|TRFTRPREDC Crithidia fasciculata trypanothione reduct... 38 4.6  
 gb|M73324|TRFTRPREDB Crithidia fasciculata trypanothione reduct... 38 4.6  
 emb|X92589|MMSEMIIGN M.mulatta semenogelin II gene 38 4.6  
 emb|Z47556|HSSG1SG2 H.sapiens genes for semenogelin I and semen... 38 4.6  
 gb|AC004753|AC004753 Homo sapiens chromosome 16. cosmid clone R... 38 4.6  
 gb|M55067|HUMNADPHO Human 47-kD autosomal chronic granulomatous... 38 4.6

gb|M73323|TRFTRPRED A Crithidia fasciculata trypanothione reduct... 38 4.6

# HUMAN ESTs

gb|R11942|R11942 yf54c05.r1 Homo sapiens cDNA clone 25950 5'. 656 0.0  
 gb|AA366384|AA366384 EST77326 Pancreas tumor III Homo sapiens c... 470 e-130  
 gb|T12566|T12566 CHR90086 Homo sapiens genomic clone P94\_24 5' ... 133 5e-29  
 gb|R37032|R37032 yf54c05.s1 Homo sapiens cDNA clone 25950 3'. 44 0.036  
 gb|AA661650|AA661650 nv02h12.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA261982|AA261982 zs20d03.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA588219|AA588219 no24c11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA250891|AA250891 zs06c06.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA244177|AA244177 nc05a02.r1 NCI\_CGAP\_Pr1 Homo sapiens cDNA ... 38 2.2  
 gb|AA715147|AA715147 nv10d05.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA659887|AA659887 nv03a10.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA627890|AA627890 nq70a08.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA603596|AA603596 np27b11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA613738|AA613738 np25h09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA715248|AA715248 nv10h06.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AI038487|AI038487 ow25d12.x1 Soares\_parathyroid\_tumor\_NbHPA ... 38 2.2  
 gb|AA252786|AA252786 zs26f10.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA287819|AA287819 zs50h04.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA564176|AA564176 nj04c08.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA643870|AA643870 np26h07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA280371|AA280371 zt05f07.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|R00687|R00687 ye78h08.r1 Homo sapiens cDNA clone 123903 5' s... 38 2.2  
 gb|AA587820|AA587820 nj06h05.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA588443|AA588443 no22c11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA568385|AA568385 nl88f06.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 38 2.2  
 gb|AA281831|AA281831 zt06c08.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA700438|AA700438 zj74b08.s1 Soares fetal liver spleen 1NFLS... 38 2.2  
 gb|AA689530|AA689530 ns66e07.r1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA688300|AA688300 nv14a09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA687962|AA687962 nv13h04.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA526586|AA526586 ni96f11.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA642589|AA642589 nq73f04.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA541594|AA541594 ni89g07.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA278713|AA278713 zs76h02.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|T58661|T58661 ya94a07.r1 Homo sapiens cDNA clone 69300 5' si... 38 2.2  
 gb|AA689473|AA689473 ns66e07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA459023|AA459023 aa26a09.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2

dbj|C76752|C76752 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 60 2e-07  
 gb|AA123048|AA123048 mn32g01.r1 Beddington mouse embryonic regi... 36 3.2  
 gb|AA616529|AA616529 vo10e01.r1 Barstead mouse myotubes MPLRB5 ... 36 3.2  
 gb|AA254370|AA254370 va13h09.r1 Soares mouse lymph node NbMLN M... 36 3.2  
 gb|AA537288|AA537288 vk46c04.r1 Soares mouse mammary gland NbMM... 36 3.2  
 gb|AA462365|AA462365 vg74c05.r1 Soares mouse NbMH Mus musculus ... 36 3.2  
 gb|AA589462|AA589462 vl47g07.s1 Stratagene mouse skin (#937313)... 36 3.2  
 gb|AA968017|AA968017 uh06h10.r1 Soares mouse hypothalamus NMHy ... 36 3.2

dbj|C93868|C93868 Dictyostelium discoideum slug cDNA, clone SSL809 36 2.8  
 gb|AA531984|AA531984 TgESTzz46b06.r1 TgME49 invivo Bradyzoite c... 36 2.8  
 gb|N60418|N60418 TgESTzy07a10.r1 TgRH Tachyzoite cDNA Toxoplasma... 36 2.8  
 gb|H32045|H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 36 2.8  
 gb|AA956789|AA956789 UI-R-E1-fr-h-01-0-UI.s1 UI-R-E1 Rattus nor... 36 2.8  
 gb|H33275|H33275 EST109117 Rat PC-12 cells, NGF-treated (9 days... 36 2.8  
 gb|AA531938|AA531938 TgESTzz45b08.r1 TgME49 invivo Bradyzoite c... 36 2.8  
 dbj|D41507|RICS4044A Rice cDNA, partial sequence (S4044\_1A). 36 2.8  
 gb|AA799411|AA799411 EST188908 Normalized rat heart, Bento Soar... 36 2.8  
 gb|AA519671|AA519671 TgESTzz27c10.r1 TgME49 invivo Bradyzoite c... 36 2.8  
 dbj|D40678|RICS2786A Rice cDNA, partial sequence (S2786\_1A). 36 2.8  
 gb|AA012430|AA012430 TgESTzz22b12.r1 TgME49cDNA Toxoplasma gond... 36 2.8  
 dbj|D40551|RICS2612A Rice cDNA, partial sequence (S2612\_1A). 36 2.8  
 gb|AI008452|AI008452 EST202903 Normalized rat embryo, Bento Soa... 36 2.8  
 dbj|D41253|RICS3620A Rice cDNA, partial sequence (S3620\_1A). 36 2.8  
 gb|AA923843|AA923843 UI-R-A1-dr-f-04-0-UI.s1 UI-R-A1 Rattus nor... 36 2.8  
 gb|AA799410|AA799410 EST188907 Normalized rat heart, Bento Soar... 36 2.8

We claim:



1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:

contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and

determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.

2. The method of claim 1, wherein the agent is selected from the group consisting of

(a)

a nucleotide acid molecule comprising NA group 1 nucleic acid molecules

or a fragment thereof,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules or a fragment thereof,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules or a fragment thereof,

(d)

an antibody that binds to an expression product of NA group 1 nucleic acids,

(e)

an antibody that binds to an expression product of NA group 3 nucleic acids,

(f)

an antibody that binds to an expression product of NA group 17 nucleic acids,

5

(g)

and agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,

10

(h)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and

15

(I)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 17 nucleic acid.

3. The method of claim 1, wherein the disorder is characterized by

expression of a plurality of human cancer associated antigen precursors and wherein the agent is  
20 a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

25 4. The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

5. A method for determining regression, progression or onset of a condition  
30 characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of

(I)

5

the protein,

(ii)

a peptide derived from the protein,

10

(iii)

an antibody which selectively binds the protein or peptide, and

(iv)

15

cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule,

as a determination of regression, progression or onset of said condition.

6.

The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.

20

7.

The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of

(a)

25

an antibody which selectively binds the protein of (I), or the peptide of (ii),

(b)

a protein or peptide which binds the antibody of (iii). and

30

(c)

a cell which presents the complex of the peptide and MHC molecule of  
(iv).

5

8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.

9. The method of claim 5, comprising assaying the sample for the peptide.

10

10. The method of claim 5, wherein the nucleic acid molecule is a NA Group 3 molecule.

11. The method of claim 5, wherein the nucleic acid molecule is a NA Group

15 11 molecule.

12. The method of claim 5, wherein the nucleic acid molecule is a NA Group 12 molecule.

20 13. The method of claim 5, wherein the nucleic acid molecule is a NA Group 13 molecule.

14. The method of claim 5, wherein the nucleic acid molecule is a NA Group 14 molecule.

25

15. The method of claim 5, wherein the nucleic acid molecule is a NA Group 15 molecule.

16. The method of claim 5, wherein the nucleic acid molecule is a NA Group

30 16 molecule.

17. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

5 18. A pharmaceutical preparation for a human subject comprising  
an agent which when administered to the subject enriches selectively the  
presence of complexes of an HLA molecule and a human cancer associated antigen, and  
a pharmaceutically acceptable carrier, wherein the human cancer  
associated antigen is a fragment of a human cancer associated antigen precursor encoded by a  
10 nucleic acid molecule comprises a NA Group 1 molecule.

19. The pharmaceutical preparation of claim 18, wherein the agent comprises  
a plurality of agents, each of which enriches selectively in the subject complexes of an HLA  
molecule and a different human cancer associated antigen.

15

20. The pharmaceutical preparation of claim 19, wherein the plurality is at  
least two, at least three, at least four or at least 5 different such agents.

21. The pharmaceutical preparation of claim 18, wherein the nucleic acid  
20 molecule is a NA Group 3 nucleic acid molecule.

22. The pharmaceutical preparation of claim 18, wherein the agent is selected  
from the group consisting of

- 25 (1) an isolated polypeptide comprising the human cancer associated  
antigen, or a functional variant thereof,  
(2) an isolated nucleic acid operably linked to a promoter for expressing  
the isolated polypeptide, or functional variant thereof.  
(3) a host cell expressing the isolated polypeptide, or functional variant  
thereof, and

(4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

23. The pharmaceutical preparation of claims 18-22, further comprising an  
5 adjuvant.

24. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.

10 25. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.

15 26. The pharmaceutical preparation of claim 18, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human cancer associated antigen or functional variant thereof.

20 27. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 2 polypeptide.

28. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

25 29. The pharmaceutical preparation of claim 25, wherein the cell expresses one or both of the polypeptide and HLA molecule recombinantly.

30 30. The pharmaceutical preparation of claim 25, wherein the cell is nonproliferative.

31. A composition comprising  
an isolated agent that binds selectively a PP Group 1 polypeptide.

32. The composition of matter of claim 31, wherein the agent binds selectively  
5 a PP Group 3 polypeptide.

33. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 11 polypeptide.

10 34. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 12 polypeptide.

35. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 13 polypeptide.

15 36. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 14 polypeptide.

37. The composition of matter of claim 31, wherein the agent binds selectively  
20 a PP Group 15 polypeptide.

38. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 16 polypeptide.

25 39. The composition of claims 31-38, wherein the agent is a plurality of  
different agents that bind selectively at least two, at least three, at least four, or at least five  
different such polypeptides.

40. The composition of claims 31-38, wherein the agent is an antibody.

30

41. The composition of claim 39, wherein the agent is an antibody.

42. A composition of matter comprising  
a conjugate of the agent of claims 31-41 and a therapeutic or diagnostic  
5 agent.

43. The composition of matter of claim 42, wherein the conjugate is of the  
agent and a therapeutic or diagnostic that is a toxin.

10 44. A pharmaceutical composition comprising an isolated nucleic acid  
molecule selected from the group consisting of:

(1)

NA Group 1 molecules, and

15

(2)

NA Group 2 molecules, and a pharmaceutically acceptable carrier.

45. The pharmaceutical composition of claim 44, wherein the isolated nucleic  
acid molecule comprises a NA Group 3 or NA Group 4 molecule.

20

46. The pharmaceutical composition of claim 44, wherein the isolated nucleic  
acid molecule comprises at least two isolated nucleic acid molecules coding for two different  
polypeptides, each polypeptide comprising a different human cancer associated antigen.

25 47. The pharmaceutical composition of claims 44-46 further comprising an  
expression vector with a promoter operably linked to the isolated nucleic acid molecule.

48. The pharmaceutical composition of claims 44-46 further comprising a host  
cell recombinantly expressing the isolated nucleic acid molecule.

30



49. A pharmaceutical composition comprising  
an isolated polypeptide comprising a PP Group 1 or a PP Group 2  
polypeptide, and  
a pharmaceutically acceptable carrier.

5

50. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

10 51. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptide comprises at least two different polypeptides, each comprising a different human  
cancer associated antigen.

52. The pharmaceutical composition of claim 49, wherein the isolated  
15 polypeptides are PP Group 11 polypeptides or HLA binding fragments thereof.

53. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptides are PP  
Group 12 polypeptides or HLA binding fragments thereof.

20

54. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptides are PP Group 13 polypeptides or HLA binding fragments thereof.

55. The pharmaceutical composition of claim 49, wherein the isolated  
25 polypeptides are PP Group 14 polypeptides or HLA binding fragments thereof.

56. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptides are PP Group 15 polypeptides or HLA binding fragments thereof.

30

57. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 16 polypeptides or HLA binding fragments thereof.

58. The pharmaceutical composition of claims 49-57, further comprising an  
5 adjuvant.

59. An isolated nucleic acid molecule comprising a NA Group 3 molecule.

60. An isolated nucleic acid molecule comprising a NA Group 4 molecule.

10 61. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 11 molecule or a fragment thereof.

62. The isolated nucleic acid molecule of claims 59-60, wherein the molecule  
15 is a Group 12 molecule or a fragment thereof.

63. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 13 molecule or a fragment thereof.

20 64. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 14 molecule or a fragment thereof.

65. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 15 molecule or a fragment thereof.

25 66. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 16 molecule or a fragment thereof.

67. An isolated nucleic acid molecule selected from the group consisting of

(a)

a fragment of a nucleic acid selected from the group of nucleic acid  
consisting of SEQ ID NOs presenting nucleic acid sequences among SEQ ID NOs. 1-816, of  
5 sufficient length to represent a sequence unique within the human genome, and identifying a  
nucleic acid encoding a human cancer associated antigen precursor,

(b)

complements of (a),

10

provided that the fragment includes a sequence of contiguous nucleotides  
which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the GenBank accession numbers of Table 1

(correct?),

15

(2) complements of (1), and

(3) fragments of (1) and (2).

68. The isolated nucleic acid molecule of claim 67, wherein the sequence of  
contiguous nucleotides is selected from the group consisting of:

20

(1)

at least two contiguous nucleotides nonidentical to the sequence group,

(2)

at least three contiguous nucleotides nonidentical to the sequence group,

(3)

25

at least four contiguous nucleotides nonidentical to the sequence group.

(4)

at least five contiguous nucleotides nonidentical to the sequence group.

(5)

30

at least six contiguous nucleotides nonidentical to the sequence group.

(6)

at least seven contiguous nucleotides nonidentical to the sequence group.

69. The isolated nucleic acid molecule of claim 67, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

70. The isolated nucleic acid molecule of claim 67, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

71. An expression vector comprising an isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70 operably linked to a promoter.

72. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.

73. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.

74. A host cell transformed or transfected with an expression vector of claims 71, 72, or 73.

75. A host cell transformed or transfected with an expression vector of claim 71 or claim 72 and further comprising a nucleic acid encoding HLA.

76. An isolated polypeptide encoded by the isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, or 66.

77. A fragment of the polypeptide of claim 76 which is immunogenic.

78. The fragment of claim 77, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

5

79. An isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

10 80. The fragment of claim 79, wherein the fragment is part of a complex with HLA.

81. The fragment of claim 79, wherein the fragment is between 8 and 12 amino acids in length.

15

82. An isolated polypeptide comprising a fragment of the polypeptide of claim 76 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

20 83. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising  
a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of

25 (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and

(b) complements of ("a"), wherein the contiguous segments are nonoverlapping.

30

84. The kit of claim 83, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

5 85. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated  
10 antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

(a)  
a nucleic acid molecule comprising NA group 1 nucleic acid molecules,

15

(b)  
a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

20

(c)  
a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

86. The method of claim 85, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes  
25 of an HLA molecule and a different human cancer associated antigen.

87. The method of claim 86, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

88. The method of claims 85-87, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

89. The method of claims 85-88, wherein the disorder is cancer.

90. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(I)  
removing an immunoreactive cell containing sample from the subject.

(ii)  
contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,

(iii)  
introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

91. The method of claim 90, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

92. The method of claim 90, wherein the host cell endogenously expresses an  
5 HLA molecule which binds the human cancer associated antigen.

93. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

10 (I)

identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule

(ii)

15 transfecting a host cell with a nucleic acid selected from the group consisting of

(a) the nucleic acid molecule identified,

20 (b)

a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen,

25 (c)

deletions, substitutions or additions to (a) or (b), and

30



(d)  
degenerates of (a), (b), or (c);

(iii)  
5 culturing said transfected host cells to express the transfected nucleic acid  
molecule, and;

(iv)  
introducing an amount of said host cells or an extract thereof to the subject  
10 effective to increase an immune response against the cells of the subject associated with the  
condition.

94. The method of claim 93, further comprising:

15 (a)  
identifying an MHC molecule which presents a portion of an expression  
product of the nucleic acid molecule.

20 wherein the host cell expresses the same MHC molecule as identified in  
(a) and wherein the host cell presents an MHC binding portion of the expression product of the  
nucleic acid molecule.

95. The method of claim 93, wherein the immune response comprises a B-cell  
25 response or a T cell response.

96. The method of claim 95, wherein the response is a T-cell response which  
comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the  
expression product of the nucleic acid molecule or cells of the subject expressing the human  
30 cancer associated antigen.

97. The method of claim 93, wherein the nucleic acid molecule is a NA Group 3 molecule.

98. The method of claims 93 or 94, further comprising treating the host cells  
5 to render them non-proliferative.

99. A method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising  
10 administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

100. The method of claim 99, wherein the antibody is a monoclonal antibody.  
15

101. The method of claim 100, wherein the monoclonal antibody is a chimeric antibody or a humanized antibody.

102. A method for treating a condition characterized by expression in a subject  
20 of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising  
administering to a subject a pharmaceutical composition of any one of claims 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 47, and 58 in an amount effective to prevent, delay the onset of, or inhibit the condition in  
25 the subject.

103. The method of claim 102, wherein the condition is cancer.

104. The method of claims 102-103, further comprising first identifying that  
30 the subject expresses in a tissue abnormal amounts of the protein.

105. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

- 5 the protein;
- (i) identifying cells from the subject which express abnormal amounts of
  - (ii) isolating a sample of the cells;
  - (iii) cultivating the cells, and
  - (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

10 106. The method of claim 105, wherein the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.

15 107. The method of claim 105, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

108. A method for treating a pathological cell condition characterized by  
20 aberrant expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising  
administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

25 109. The method of claim 108, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

110. The method of claim 108, wherein the agent is an antisense nucleic acid  
30 molecule which selectively binds to the nucleic acid molecule which encodes the protein.

111. The method of claim 108, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

112. A composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules, comprising

a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

113. The composition of matter of claim 112, wherein at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto.

114. The composition of matter of claim 113, further comprising an adjuvant.

115. The composition of matter of claim 114, wherein said adjuvant is a saponin, GM-CSF, or an interleukin.

116. An isolated antibody which selectively binds to a complex of:

(i)

a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and

(ii)

and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (i) or (ii) alone.

117. The antibody of claim 116, wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

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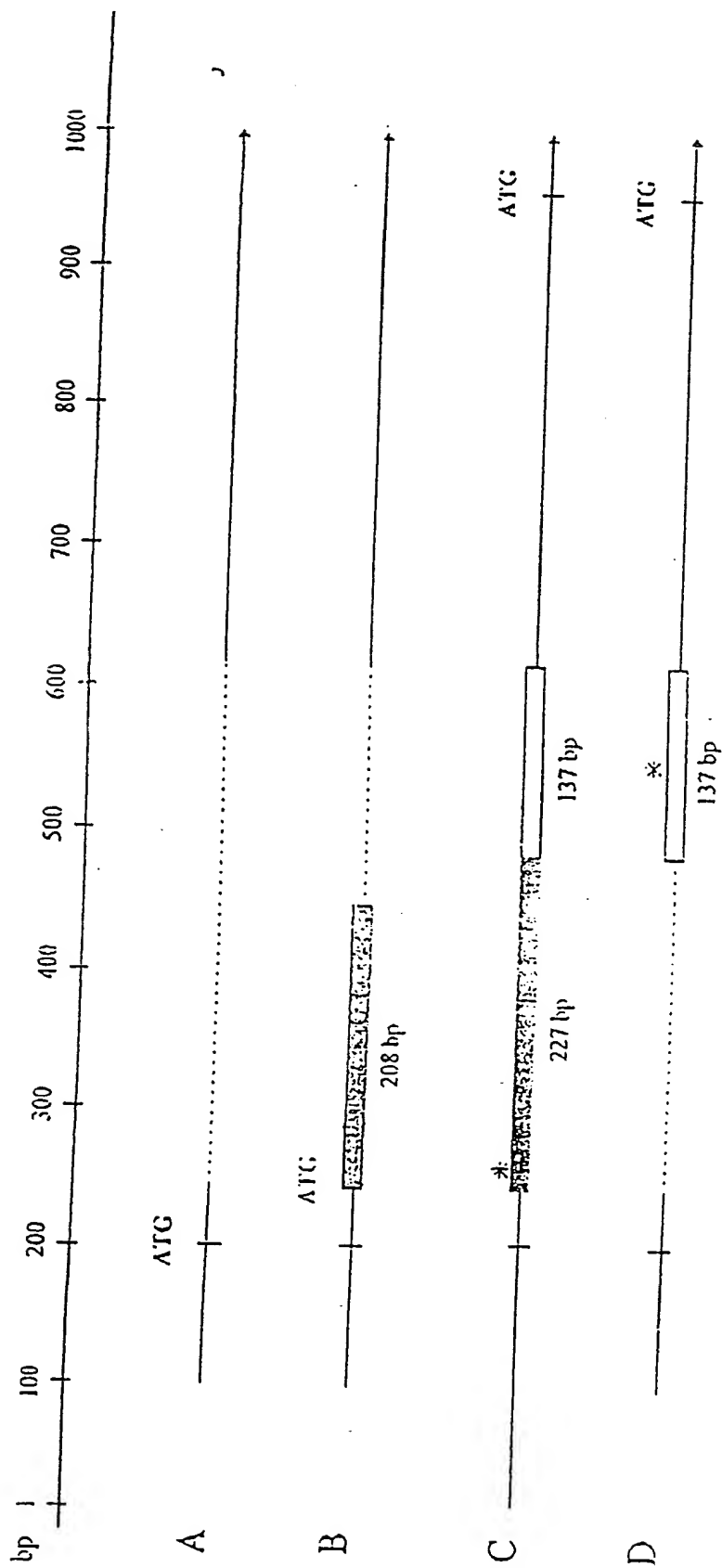
*Figure 1*





Fig 2 (cont'd)





### Transcript Variant B

[illegible]

Fig. 3a

## Figure 3b.

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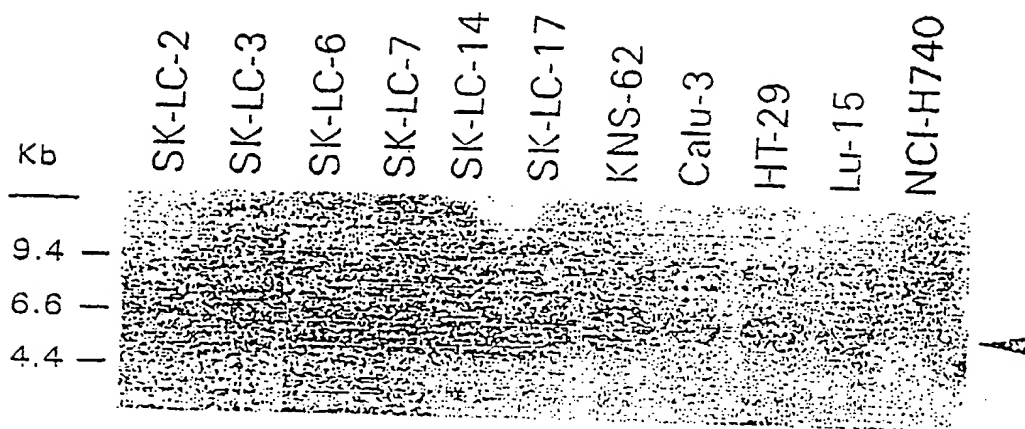


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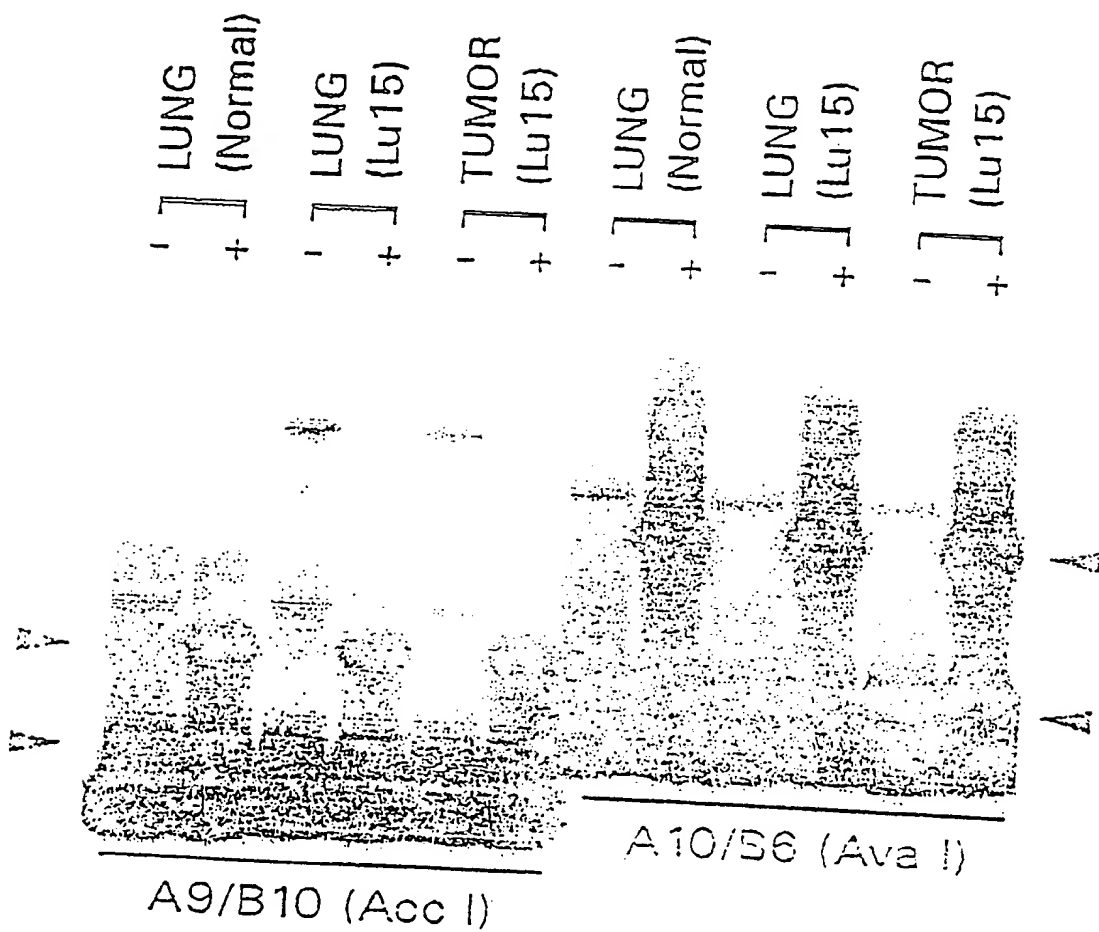


Figure 5

## SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research  
Old, Lloyd J.  
Scanlan, Matthew J.  
Stockert, Elisabeth  
Gure, Ali  
Chen, Yao-Tseng  
Gout, Ivan  
O'Hare, Michael  
Obata, Yuichi  
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&lt;211&gt; 850

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&lt;213&gt; Homo Sapiens

&lt;400&gt; 12

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&lt;211&gt; 1113

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 16

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&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 17

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&lt;210&gt; 26

&lt;211&gt; 374

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 26

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&lt;210&gt; 27

&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 27

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&lt;210&gt; 28

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 28

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 <213> Homo Sapiens

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&lt;210&gt; 31

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 31

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&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

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&lt;210&gt; 40

&lt;211&gt; 619

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 40

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&lt;210&gt; 41

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 41

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 20              25              30
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 35              40              45
Pro Leu Glu Gly Arg Asn Thr Glu Asp Ser Tyr Ser Leu Ala Pro Trp
 50              55              60
Gln Gln Gln Gln Ile Glu Phe Arg Gln Gly Ser Glu Thr Pro Met Gln
 65              70              75              80
Val Leu Thr Gly Ser Ser Arg Gln Ser Tyr Ser Pro Gly Tyr Gln Asp
 85              90              95
Phe Ser Lys Trp Glu Ser Met Leu Lys Lys Glu Gly Leu Leu Arg Gln
 100             105             110
Lys Glu Ile Val Asp Arg Gln Lys Gln Ile Thr His Leu Ile Arg Asp
 115             120             125
Asn Glu Leu Pro Ala His Ala Met Leu Gly His Tyr Val Asn Cys Glu
 130             135             140

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Asp Ser Tyr Val Ala Ser Leu His His  
145 150

<210> 42  
<211> 95  
<212> PRT  
<213> Homo Sapiens

<400> 42  
Ile Leu Leu Glu Phe Tyr Leu Trp Gln Ile Gly Arg Tyr Ile Phe Val  
1 5 10 15  
His Val Asn Asn His Ile Tyr Ile Lys Leu Tyr Asn Cys Thr Phe Leu  
20 25 30  
Thr Ala Leu Ser Gln Val Ala Leu Ser Phe Pro Ser Ile Asn Gly Leu  
35 40 45  
Ile Phe Val Ser Phe Ala Phe Phe Arg Val Val Asn Ser Tyr Cys Pro  
50 55 60  
Leu Gln Phe Val Gln Phe Leu Arg Cys Leu Leu Leu Lys Arg Met  
65 70 75 80  
Leu Gly Glu Phe Ile Phe His Lys Glu Met Glu His Tyr Leu Lys  
85 90 95

<210> 43  
<211> 114  
<212> PRT  
<213> Homo Sapiens

<400> 43  
Ser Lys Leu Leu Leu Ser Gly Thr Ala Asp Gly Ala Asp Leu Arg Thr  
1 5 10 15  
Val Asp Pro Glu Thr Gln Ala Arg Leu Glu Ala Leu Leu Glu Ala Ala  
20 25 30  
Gly Ile Gly Lys Leu Ser Thr Ala Asp Gly Lys Ala Phe Ala Asp Pro  
35 40 45  
Glu Val Leu Arg Arg Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu  
50 55 60  
Ala Ala Ala Leu Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly  
65 70 75 80  
Gln Ser Asp Asn Arg Ser Leu Ala Glu Ala Cys Ser Gly Asp Val Ala  
85 90 95  
Val Arg Lys Leu Leu Ile Glu Gly Arg Ser Val Phe Glu Leu Pro Glu  
100 105 110  
Glu Gly

<210> 44  
<211> 132  
<212> PRT  
<213> Homo Sapiens

<400> 44  
Gly Glu Lys Glu Gln Asp Lys Pro Pro Asn Leu Val Leu Lys Asp Lys  
1 5 10 15  
Val Lys Pro Lys Gln Asp Thr Lys Tyr Asp Leu Ile Leu Asp Glu Gln  
20 25 30

Ala Glu Asp Ser Lys Ser Ser His Ser His Thr Ser Lys His Lys Lys  
 35 40 45  
 Lys Thr His His Cys Ser Glu Lys Glu Asp Glu Asp Tyr Met Pro  
 50 55 60  
 Ile Lys Asn Thr Asn Gln Asp Ile Tyr Arg Glu Met Gly Phe Gly His  
 65 70 75 80  
 Tyr Glu Glu Glu Glu Ser Cys Trp Glu Lys Gln Lys Ser Glu Lys Arg  
 85 90 95  
 Asp Arg Thr Gln Asn Arg Ser Arg Ser Arg Ser Arg Glu Arg Asp Gly  
 100 105 110  
 His Tyr Ser Asn Ser His Lys Ser Lys Tyr Gln Thr Asp Leu Tyr Glu  
 115 120 125  
 Arg Glu Arg Ser  
 130

<210> 45  
 <211> 214  
 <212> PRT  
 <213> Homo Sapiens

<400> 45  
 Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu  
 1 5 10 15  
 Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile  
 20 25 30  
 Gln Arg Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys  
 35 40 45  
 Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg  
 50 55 60  
 Ser Arg Lys Ala Val Ser Lys Leu Ala Ser Lys Ala His Met Asn Ser  
 65 70 75 80  
 Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala Gly  
 85 90 95  
 Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu Val  
 100 105 110  
 Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu Met  
 115 120 125  
 Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu Ser  
 130 135 140  
 Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile Asp  
 145 150 155 160  
 Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro Ser  
 165 170 175  
 Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Pro Gly Ala Met Ala  
 180 185 190  
 Ala Ser Glu Asp Glu Glu Glu Glu Glu Leu Glu Ala Met Gln Ser  
 195 200 205  
 Arg Leu Ala Thr Arg Ser  
 210

<210> 46  
 <211> 248  
 <212> PRT  
 <213> Homo Sapiens

&lt;400&gt; 46

Gly Ser Arg Glu Glu Thr Leu Ala Phe Val Pro Leu Leu Arg Leu Leu  
 1 5 10 15  
 Glu Ala Thr Leu Ser Pro Gly Arg Ala Phe Cys Ser Pro Ile Ser Ser  
 20 25 30  
 Lys Ile Gln Pro Ala Gln Val Ala Gly His Glu Leu Cys Ser Gly Ser  
 35 40 45  
 Trp Asn Leu Thr Leu Val Ala Ser Gly Pro Val Ser Met Ala Ala Glu  
 50 55 60  
 His Leu Leu Pro Gly Pro Pro Pro Ser Leu Ala Asp Phe Leu Glu Ala  
 65 70 75 80  
 Gly Gly Lys Gly Thr Glu Arg Gly Ser Gly Ser Ser Lys Pro Thr Gly  
 85 90 95  
 Ser Ser Gly Gly Pro Arg Met Ala Ser Phe Pro Lys Thr Lys Phe Asn  
 100 105 110  
 Glu Tyr Lys Asp Val Leu Pro Cys Met Thr Ser Ser Arg Gly Gly Lys  
 115 120 125  
 Ile Lys Ala Thr Asp Phe Met Val Ala Met Arg Cys Leu Gly Ala Ser  
 130 135 140  
 Pro Thr Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp  
 145 150 155 160  
 Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met  
 165 170 175  
 Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu  
 180 185 190  
 Met Val Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg  
 195 200 205  
 Ser Lys Leu Thr Ser Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp  
 210 215 220  
 Leu Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp  
 225 230 235 240  
 Glu Phe Ile His Lys Ile Thr Leu  
 245

&lt;210&gt; 47

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 47

Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys Trp Asn Glu Tyr Leu  
 1 5 10 15  
 Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn Cys Thr Cys Pro Ile  
 20 25 30  
 Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe Ile Arg Ala Ile Val  
 35 40 45  
 Ser Ser Pro Glu Val Ile Ser Lys Tyr Lys Ala Leu Leu Arg Gly Tyr  
 50 55 60  
 Val Glu Ser Cys Ser Asn Leu Thr Trp Cys Thr Asn Pro Gln Gly Cys  
 65 70 75 80  
 Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly Cys Gly Thr Thr Cys Ser  
 85 90 95  
 Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys Ser Phe Pro Glu Ala His  
 100 105 110  
 Tyr Pro Ala Ser Cys Gly His Met Ser Gln Trp Val Asp Asp Gly Gly

115 120 125  
 Tyr Tyr Asp Gly Met Ser Val Glu Ala Lys His Leu Ala Lys Leu Ile  
 130 135 140  
 Ser Lys Arg Cys Pro Ser Cys Gln Ala Pro Ile Glu Asn Glu Gly Cys  
 145 150 155 160  
 Leu His Met Thr Cys Ala Lys Cys Asn His Gly Phe Cys Trp Arg Cys  
 165 170 175  
 Leu

<210> 48  
 <211> 102  
 <212> PRT  
 <213> Homo Sapiens

<400> 48  
 Glu Lys Gly Leu His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala  
 1 5 10 15  
 Gln Lys Gly Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly  
 20 25 30  
 Gly Val Ala Cys Thr Thr Thr Val Leu Ser Cys Leu His Leu Leu Ser  
 35 40 45  
 Gln Gly Tyr Lys Arg Asp Arg Pro Gln Ile Leu Met Tyr Ala Ala Pro  
 50 55 60  
 Pro Met Gly Pro Cys Arg Gly Ala His Phe Cys Gly Ser Ser Gln Thr  
 65 70 75 80  
 Ser Pro Pro Lys Pro Val Ala Thr Leu Ser Leu Leu Pro Cys Pro Leu  
 85 90 95  
 Pro Pro Leu Lys Asn Gly  
 100

<210> 49  
 <211> 179  
 <212> PRT  
 <213> Homo Sapiens

<400> 49  
 His Lys Pro Cys Asn Pro Arg Glu Lys Glu Arg Ile Gln Asn Ala Gly  
 1 5 10 15  
 Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala Val Ser Arg  
 20 25 30  
 Ala Leu Gly Asp Tyr Asp Tyr Lys Cys Val Asp Gly Lys Gly Pro Thr  
 35 40 45  
 Glu Gln Leu Val Ser Pro Glu Pro Glu Val Tyr Glu Ile Leu Arg Ala  
 50 55 60  
 Glu Glu Asp Glu Phe Ile Ile Leu Ala Cys Asp Gly Ile Trp Asp Val  
 65 70 75 80  
 Met Ser Asn Glu Glu Leu Cys Glu Tyr Val Lys Ser Arg Leu Glu Val  
 85 90 95  
 Ser Asp Asp Leu Glu Asn Val Cys Asn Trp Val Val Asp Thr Cys Leu  
 100 105 110  
 His Lys Gly Ser Arg Asp Asn Met Ser Ile Val Leu Val Cys Phe Ser  
 115 120 125  
 Asn Ala Pro Lys Val Ser Asp Glu Ala Val Lys Lys Asp Ser Glu Leu  
 130 135 140



Asp Lys His Leu Glu Ser Ile Met Glu Asn Leu Ala Lys Glu Cys Leu  
 145 150 155 160  
 Ile Leu Pro Met Ser Cys Ala Ser Cys Leu Gln Lys Ile Ser Gln Ile  
 165 170 175  
 Cys Leu Leu

<210> 50  
 <211> 163  
 <212> PRT  
 <213> Homo Sapiens

<400> 50  
 Asp Leu Pro Thr Leu Glu Asp His Gln Lys Gln Ser Gln Gln Leu Lys  
 1 5 10 15  
 Asp Ser Glu Leu Lys Ser Thr Glu Leu Gln Glu Lys Val Thr Glu Leu  
 20 25 30  
 Glu Ser Leu Leu Glu Glu Thr Gln Ala Ile Cys Arg Glu Lys Glu Ile  
 35 40 45  
 Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala Glu Phe Ser Ser Ala Gly  
 50 55 60  
 His Ser Leu Gln Asp Lys Gln Ser Val Glu Glu Thr Ser Gly Glu Gly  
 65 70 75 80  
 Pro Glu Val Glu Met Glu Ser Trp Gln Lys Arg Tyr Asp Ser Leu Gln  
 85 90 95  
 Lys Ile Val Glu Lys Gln Gln Gln Lys Met Asp Gln Leu Arg Ser Gln  
 100 105 110  
 Val Gln Ser Leu Glu Gln Glu Val Ala Glu Glu Gly Thr Ser Gln Ala  
 115 120 125  
 Leu Arg Glu Glu Ala Gln Arg Arg Asp Ser Ala Leu Gln Gln Leu Arg  
 130 135 140  
 Thr Ala Val Lys Leu Ser Val Asn Gln Asp Leu Ile Glu Lys Asn Leu  
 145 150 155 160  
 Thr Leu Gln

<210> 51  
 <211> 164  
 <212> PRT  
 <213> Homo Sapiens

<400> 51  
 Phe Gly Asp Ser Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys  
 1 5 10 15  
 Phe Ile Glu Glu Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu  
 20 25 30  
 Asn Arg Lys Asn Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe  
 35 40 45  
 Ile Ser Pro Phe Gly Arg Gly Leu Arg Pro Leu Ala Phe Leu Arg Ala  
 50 55 60  
 Val His Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu  
 65 70 75 80  
 Met Pro Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu  
 85 90 95  
 Lys Glu Glu Glu Ile His Ile Tyr Gln Phe Phe Glu Cys Asp Ser Asp

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          100          105          110
Glu Asp Glu Asp Phe Lys Arg Gln Asp Ala Met Lys Glu Ser Ile Pro
          115          120          125
Phe Ala Val Val Gly Ser Cys Gln Val Val Arg Asp Gly Gly Asn Arg
          130          135          140
Pro Val Arg Gly Arg Arg Tyr Ser Trp Gly Asn Val Glu Val Asn His
          145          150          155          160
Ile Ala Ile Ser

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<210> 52
<211> 600
<212> PRT
<213> Homo Sapiens

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          <400> 52
Met Cys Pro Arg Gln Val Asp Arg Ala Lys Glu Lys Gly Ile Gly Thr
  1          5          10          15
Pro Gln Pro Asp Val Ala Lys Asp Ser Trp Ala Glu Leu Glu Asn Ser
          20          25          30
Ser Lys Glu Asn Glu Val Ile Glu Val Lys Ser Met Gly Glu Ser Gln
          35          40          45
Ser Lys Lys Leu Gln Gly Gly Tyr Glu Cys Lys Tyr Cys Pro Tyr Ser
          50          55          60
Thr Gln Asn Leu Asn Glu Phe Thr Glu His Val Asp Met Gln His Pro
          65          70          75          80
Asn Val Ile Leu Asn Pro Leu Tyr Val Cys Ala Glu Cys Asn Phe Thr
          85          90          95
Thr Lys Lys Tyr Asp Ser Leu Ser Asp His Asn Ser Lys Phe His Pro
          100          105          110
Gly Glu Ala Asn Phe Lys Leu Lys Leu Ile Lys Arg Asn Asn Gln Thr
          115          120          125
Val Leu Glu Gln Ser Ile Glu Thr Thr Asn His Val Val Ser Ile Thr
          130          135          140
Thr Ser Gly Pro Gly Thr Gly Asp Ser Asp Ser Gly Ile Ser Val Ser
          145          150          155          160
Lys Thr Pro Ile Met Lys Pro Gly Lys Pro Lys Ala Asp Ala Lys Lys
          165          170          175
Val Pro Lys Lys Pro Glu Glu Ile Thr Pro Glu Asn His Val Glu Gly
          180          185          190
Thr Ala Arg Leu Val Thr Asp Thr Ala Glu Ile Leu Ser Arg Leu Gly
          195          200          205
Gly Val Glu Leu Leu Gln Asp Thr Leu Gly His Val Met Pro Ser Val
          210          215          220
Gln Leu Pro Pro Asn Ile Asn Leu Val Pro Lys Val Pro Val Pro Leu
          225          230          235          240
Asn Thr Thr Lys Tyr Asn Ser Ala Leu Asp Thr Asn Ala Thr Met Ile
          245          250          255
Asn Ser Phe Asn Lys Phe Pro Tyr Pro Thr Gln Ala Glu Leu Ser Trp
          260          265          270
Leu Thr Ala Ala Ser Lys His Pro Glu Glu His Ile Arg Ile Trp Phe
          275          280          285
Ala Thr Gln Arg Leu Lys His Gly Ile Ser Trp Ser Pro Glu Glu Val
          290          295          300
Glu Glu Ala Arg Lys Lys Met Phe Asn Gly Thr Ile Gln Ser Val Pro

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```
<210> 53
<211> 163
<212> PRT
<213> Homo Sapiens
```

<400> 53															
Arg	Lys	Ser	Trp	Glu	His	Lys	Glu	Glu	Ile	Ser	Glu	Ala	Glu	Pro	Gly
1				5					10					15	
Gly	Gly	Ser	Leu	Gly	Asp	Gly	Arg	Pro	Pro	Glu	Glu	Ser	Ala	His	Glu
			20					25					30		
Met	Met	Glu	Glu	Glu	Glu	Glu	Ile	Pro	Lys	Pro	Lys	Ser	Val	Val	Ala
		35					40					45			
Pro	Pro	Gly	Ala	Pro	Lys	Lys	Glu	His	Val	Asn	His	Val	Ala	Gly	Lys
	50					55				60					
Ser	Thr	Ile	Gly	Gly	Gln	Ile	Met	Tyr	Leu	Thr	Gly	Met	Val	Asp	Lys
65				70						75					80
Arg	Thr	Leu	Glu	Lys	Tyr	Glu	Arg	Glu	Ala	Lys	Glu	Lys	Asn	Arg	Glu

```

      85              90              95
Thr Trp Tyr Leu Ser Trp Ala Leu Asp Thr Asn Gln Glu Glu Arg Asp
      100              105              110
Lys Gly Lys Thr Val Glu Val Gly Arg Ala Tyr Phe Glu Thr Glu Lys
      115              120              125
Lys His Phe Thr Ile Leu Asp Met Asn Pro Arg Thr Leu Ser Ser Lys
      130              135              140
Pro Lys Ala Gln Asn Leu Lys Leu Lys Val Pro Asn Ser Lys Val Arg
      145              150              155              160
Arg Cys Phe

```

<210> 54  
 <211> 155  
 <212> PRT  
 <213> Homo Sapiens

```

      <400> 54
Glu Arg Trp Pro Glu Glu Gly Thr Ala Asp Leu Ala Gln Ser Gly Leu
  1              5              10              15
Glu Gly Gly Thr Thr Arg Ala Ser Val Ser Trp Cys Cys Leu Glu Gly
      20              25              30
Ser Trp Leu Leu Ser Gly Tyr Leu Thr Phe Leu Lys Thr Cys Ser His
      35              40              45
Thr Ala Ser Leu Ala Val Ser Ser Ser Cys Arg Ile Arg His Glu
      50              55              60
Leu Val Pro Asn Ser Ala Arg Gly Lys His Tyr Ser Gln Arg Trp Ala
      65              70              75              80
Gln Glu Asp Leu Leu Glu Glu Gln Lys Asp Gly Ala Arg Ala Ala Ala
      85              90              95
Val Ala Asp Lys Lys Lys Gly Leu Met Gly Pro Leu Thr Glu Leu Asp
      100              105              110
Thr Lys Asp Val Asp Ala Leu Leu Lys Lys Ser Glu Ala Gln His Glu
      115              120              125
Gln Pro Glu Asp Gly Cys Pro Phe Gly Ala Leu Thr Gln Arg Leu Leu
      130              135              140
Gln Ala Leu Val Glu Glu Asn Ile Ile Phe Ser
      145              150              155

```

<210> 55  
 <211> 112  
 <212> PRT  
 <213> Homo Sapiens

```

      <400> 55
Ser Glu Arg Ala Leu Ala Pro Arg Thr Tyr Arg Met Glu Thr Ala Arg
  1              5              10              15
Ser Ala Pro Tyr Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro
      20              25              30
Asp Leu Ala Ala Gln Met Met Leu Asn Ser Pro Leu Phe Thr Ala Asn
      35              40              45
Pro Gln Leu Gln Glu Gln Met Arg Pro Gln Leu Pro Ala Phe Leu Gln
      50              55              60
Gln Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala
      65              70              75              80

```

Met Gln Ala Leu Met Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr  
                     85                    90                    95  
 Glu Ala Pro Gly Leu Ile Pro Ser Phe Thr Pro Gly Val Gly Val Gly  
                     100                    105                    110

<210> 56  
 <211> 151  
 <212> PRT  
 <213> Homo Sapiens

<400> 56  
 Lys Phe Gly Met Pro Ile Asp Cys Gly Leu Pro Pro His Ile Asp Phe  
   1                    5                    10                    15  
 Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln Gly Tyr Phe Glu Gln Glu  
                     20                    25                    30  
 Asp Asp Met Met Glu Val Pro Tyr Val Thr Pro His Pro Pro Tyr His  
                     35                    40                    45  
 Leu Gly Ala Val Ala Lys Thr Trp Glu Asn Thr Lys Glu Ser Pro Ala  
   50                    55                    60  
 Thr His Ser Ser Asn Phe Leu Tyr Gly Thr Met Val Ser Tyr Thr Cys  
  65                    70                    75                    80  
 Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro Val Leu Ile Cys Gln Glu  
                     85                    90                    95  
 Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser Cys Ile Ser Ile Glu Cys  
                     100                    105                    110  
 Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe Leu Arg Phe Thr Glu Thr  
                     115                    120                    125  
 Ser Met Gly Ser Ala Val Gln Tyr Ser Cys Lys Pro Gly His Ile Leu  
  130                    135                    140  
 Ala Gly Ser Asp Leu Arg Leu  
 145                    150

<210> 57  
 <211> 220  
 <212> PRT  
 <213> Homo Sapiens

<400> 57  
 Ala Ala Phe Val Ser Glu Val Thr Ser Phe Pro Val Val Gln Leu His  
   1                    5                    10                    15  
 Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser  
                     20                    25                    30  
 Ile Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys  
                     35                    40                    45  
 Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn  
   50                    55                    60  
 Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp  
  65                    70                    75                    80  
 Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn  
                     85                    90                    95  
 Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser  
                     100                    105                    110  
 Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu  
                     115                    120                    125  
 Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro

```

      130              135              140
Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg
145              150              155              160
Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr
      165              170              175
Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr
      180              185              190
Asp Ile Pro Pro Gly Gly Val Glu Lys Ala Lys Asn Asn Ala Val Leu
      195              200              205
Leu Lys Gly Ile Cys Gly Leu Phe Tyr Arg Ile Ser
      210              215              220

```

<210> 58  
 <211> 101  
 <212> PRT  
 <213> Homo Sapiens

```

      <400> 58
Trp Pro Asp Leu Val His Thr Trp Ser Ser Glu Glu Ala Met Gly Ser
  1              5              10              15
Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn His Arg Asn
      20              25              30
Lys Phe Lys Val Ile Asn Val Asp Asp Gly Asn Glu Leu Gly Ser
      35              40              45
Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr Thr Arg Lys
      50              55              60
Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr
      65              70              75              80
Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Pro Arg Cys Gln Thr Gly
      85              90              95
Thr Arg Asn Leu Cys
      100

```

<210> 59  
 <211> 43  
 <212> PRT  
 <213> Homo Sapiens

```

      <400> 59
Ala His Gly Pro Gly Val Glu Pro Thr Ser Arg His Gln Lys Asn Asn
  1              5              10              15
Leu Ser Ser Ser His Thr Val Arg Leu Glu Thr Arg Gly Gln Thr Glu
      20              25              30
Asn Gln Glu Cys Leu Leu Cys Pro His Glu Glu
      35              40

```

<210> 60  
 <211> 210  
 <212> PRT  
 <213> Homo Sapiens

```

      <400> 60
Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu Gly Ile
  1              5              10              15
Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser Lys Asp

```

20 25 30  
 Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr Ala Asn  
 35 40 45  
 Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys Asn Leu  
 50 55 60  
 Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys Leu Glu  
 65 70 75 80  
 Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln Phe Lys  
 85 90 95  
 Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly Glu Leu  
 100 105 110  
 Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu Val Glu  
 115 120 125  
 Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln Asn Ile  
 130 135 140  
 Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala Ala Arg  
 145 150 155 160  
 Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser Asn Ser  
 165 170 175  
 Leu Pro Gly Leu Met Met Leu Arg Asn Lys Gly Val Ser Glu Lys Tyr  
 180 185 190  
 Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys Thr Ser Gln  
 195 200 205  
 Arg Lys  
 210

<210> 61  
 <211> 40  
 <212> PRT  
 <213> Homo Sapiens

<400> 61  
 Thr Pro Gly Pro Gly Ala Gly Phe Tyr Ala Cys Pro Ala Arg Pro Leu  
 1 5 10 15  
 Val Ser Gly Ile Tyr Ser Phe Arg Trp Val Arg Gly Leu Ala Asp Gln  
 20 25 30  
 Glu Arg Asn Trp Gly Leu Ser Gln  
 35 40

<210> 62  
 <211> 238  
 <212> PRT  
 <213> Homo Sapiens

<400> 62  
 His Glu Ala Arg Leu Lys Arg Ala Ser Ala Pro Thr Phe Asp Asn Asp  
 1 5 10 15  
 Tyr Ser Leu Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Val Ser Gln  
 20 25 30  
 Ala Val Glu Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys  
 35 40 45  
 Leu Pro Ser Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val  
 50 55 60  
 Asp Ser Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg  
 65 70 75 80

Glu Pro Ser Thr Ser Asp Leu Gly Thr Thr Asp Val Gln Lys Lys Lys  
                   85                                  90                  95  
 Leu Val Asp Ala Ile Val Ser Gly Asp Thr Ser Lys Leu Met Lys Ile  
                   100                                  105                  110  
 Leu Gln Pro Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu  
                   115                                  120                  125  
 Leu His Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu  
                   130                                  135                  140  
 Leu Leu Asn Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr  
 145                                  150                                  155                  160  
 Pro Leu His Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu  
                   165                                  170                  175  
 Leu Leu Ala Arg Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr  
                   180                                  185                  190  
 Ala Leu His Phe Ala Asn Gly Gly Val His Thr Ala Ala Val Gly Glu  
                   195                                  200                  205  
 Arg Leu Gly Gln Thr Lys Val Asp Phe Glu Gly Arg Thr Pro Met Gln  
 210                                  215                                  220  
 Val Gly Leu Pro Thr Thr Gly Lys Asn Ile Leu Arg Ile Leu  
 225                                  230                                  235

<210> 63  
 <211> 146  
 <212> PRT  
 <213> Homo Sapiens

<400> 63  
 Arg Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly Pro Asp Phe  
 1                                  5                                  10                  15  
 Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu Gln  
                   20                                  25                  30  
 Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu Arg  
                   35                                  40                  45  
 Asp Lys Val Lys Phe Thr Val His Thr Lys Ile Pro Pro Ala Pro Pro  
 50                                  55                                  60  
 Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu  
 65                                  70                                  75                  80  
 Gly Glu Gly Ser Met Thr Lys Glu Glu Phe Thr Lys Met Lys Gln Glu  
                   85                                  90                  95  
 Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His  
                   100                                  105                  110  
 Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp  
                   115                                  120                  125  
 Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg  
                   130                                  135                  140  
 Gly Lys  
 145

<210> 64  
 <211> 63  
 <212> PRT  
 <213> Homo Sapiens

<400> 64  
 Glu Arg Gly His Ser Ile Lys Asp Phe Val Ser Phe Ala Arg His Phe



1		5		10		15									
Ser	Pro	Asn	Pro	Arg	Ile	Val	Ser	Val	Asn	Ala	Ser	Tyr	Ser	Leu	Ser
		20						25					30		
Asn	Glu	Ser	Ser	Leu	Glu	Gln	Val	Tyr	Thr	Leu	Lys	Met	Ser	Phe	Ile
		35					40					45			
Ala	Ser	Asn	Thr	Tyr	His	Asn	Gln	Leu	Tyr	Lys	Glu	Gly	Phe	Leu	
	50					55					60				

&lt;210&gt; 65

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 65

Glu	Ala	Pro	Asp	Ser	Ala	Glu	Gly	Thr	Thr	Leu	Thr	Val	Leu	Pro	Glu
1				5				10					15		
Gly	Glu	Glu	Leu	Pro	Leu	Cys	Val	Ser	Glu	Ser	Asn	Gly	Leu	Glu	Leu
		20						25				30			
Pro	Pro	Ser	Ala	Ala	Ser	Asp	Glu	Pro	Leu	Gln	Glu	Pro	Leu	Glu	Ala
		35				40					45				
Asp	Arg	Thr	Ser	Glu	Glu	Leu	Thr	Glu	Ala	Lys	Thr	Pro	Thr	Ser	Ser
	50					55				60					
Pro	Glu	Lys	Pro	Gln	Glu	Leu	Val	Thr	Ala	Glu	Val	Ala	Ala	Pro	Ser
65				70					75					80	
Thr	Ser	Ser	Ser	Ala	Thr	Ser	Ser	Pro	Glu	Gly	Pro	Ser	Pro	Ala	Arg
				85				90					95		
Pro	Pro	Arg	Arg	Arg	Thr	Ser	Ala	Asp	Val	Glu	Ile	Arg	Gly	Gln	Gly
		100						105					110		
Thr	Gly	Arg	Pro	Gly	Gln	Pro	Pro	Gly	Pro	Lys	Val	Leu	Arg	Lys	Leu
	115					120						125			
Pro	Gly	Arg	Leu	Val	Thr	Val	Val	Glu	Glu	Lys	Glu	Leu	Val	Arg	Arg
	130					135				140					
Arg	Arg	Gln	Gln	Arg	Gly	Ala	Ala	Ser	Thr	Leu	Val	Pro	Gly	Val	Ser
145				150				155					160		
Glu	Thr	Ser	Ala	Ser	Pro	Gly	Ser	Pro	Ser	Val	Arg	Ser	Met	Ser	Gly
			165					170					175		
Pro	Glu	Ser	Ser	Pro	Pro	Ile	Gly	Gly	Pro	Cys	Glu	Ala	Ala	Pro	Ser
		180					185					190			
Ser	Ser	Leu	Pro	Thr	Pro	Pro									
		195													

&lt;210&gt; 66

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 66

ttctttgaaa	cattattatt	cagaacgaag	gagaatgata	cagatacact	ggctgagggtg	60
ttttgagggtg	cattgaaatg	ttccatgctg	ttacttaggt	taacatgttc	ttgagggtacc	120
atgccatgga	ttaaaaggaa	atttggttaag	tggcttcac	ctaaacgact	tactagggaa	180
gctatgcgaa	attatttaaa	agggttaagg	gatcaaatag	tacttatcct	tcatgcaaaa	240
gttgtagaga	agtcatatgg	caatcaaaaa	attttttttt	gccctcccc	ttgtgtatat	300
cttatgggca	gtggatggaa	gaaaaaaaaa	gaacaaatga	aatgcatgg	ttgttctgaa	360
cacagctctc	atccatgtgc	atttattggg	ataggaaata	gtgaccaaga	aatgcagcag	420
ctaaacttgg	aaggaaagaa	ctattgcaca	gccaaaacat	tgtacatatc	tgattcagac	480

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aagcaaaagc acttcatttt ttctgtaaag gtgttctatg gcaacgggtga tgacattgggt 540
gtgttcctca gcaagtagat aaaagtcata tccaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgtctcagga acaaagggtg ctctgtttaa tcgactacga 660
tcccagacag ttagtaccag atacttgcac gtagaaggag gtaattttca tgccagttca 720
cagcagtggg gagcatttta cattcaattc ttggatgatg atggatcaga aggagaagaa 780
ttcacagtct gagatgccta cattcattat ggacaaacat gcaaacttgt gtgctcagtt 840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcac ttaccttaa ggatacagaa 960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca 1020
agagaaccaa ataaagagat gataaatgat ggcgcttctt ggacaatcat tagcacagat 1080
aaggcagggg atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg 1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca 1200
ggacagaatt tcaactccaa ttacagagtg tggtttgggg gggtagaagc tgaaactatg 1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca ttcttgcatt ccgagaaggt 1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tgggtccgaaa tgatggaatc 1380
atattattcca ccagccttac ctttacctac acaccagaac cagggcccgcg gccacattgc 1440
agtgcagcag gagcaatcct tctagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
acaaacagcg agggaagtta cacaaacgcc agcacaaatt caaccagtgt cacatcatct 1560
acagccacag tggatccta actaccgtct ttttgtctag 1599

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&lt;210&gt; 67

&lt;211&gt; 729

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 67

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Met Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val
1           5           10           15
Ile Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp
           20           25           30
Leu Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile
           35           40           45
Ala Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys
           50           55           60
Leu Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu Asp Leu Ala Glu
65           70           75           80
Thr Leu Lys Lys Glu Lys Leu Lys Val Lys Gly Pro Ala Leu Ser Arg
           85           90           95
Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser Thr Ser
           100          105          110
Ser Thr Val Lys Thr Glu Gly Ala Glu Ala Thr Pro Gly Ala Gln Lys
           115          120          125
Arg Lys Lys Ser Thr Lys Glu Lys Ala Gly Pro Lys Gly Ser Lys Val
           130          135          140
Ser Glu Glu Gln Thr Gln Pro Pro Ser Pro Ala Gly Ala Gly Met Ser
145          150          155          160
Thr Ala Met Gly Arg Ser Pro Ser Pro Lys Thr Ser Leu Ser Ala Pro
           165          170          175
Pro Asn Ser Ser Ser Thr Glu Asn Pro Lys Thr Val Ala Lys Cys Gln
           180          185          190
Val Thr Pro Arg Arg Asn Val Leu Gln Lys Arg Pro Val Ile Val Lys
           195          200          205
Val Leu Ser Thr Thr Lys Pro Phe Glu Tyr Glu Thr Pro Glu Met Glu
           210          215          220
Lys Lys Ile Met Phe His Ala Thr Val Ala Thr Gln Thr Gln Phe Phe

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225					230					235				240
His	Val	Lys	Val	Leu	Asn	Thr	Ser	Leu	Lys	Glu	Lys	Phe	Asn	Gly
				245					250					255
Lys	Ile	Ile	Ile	Ile	Ser	Asp	Tyr	Leu	Glu	Tyr	Asp	Ser	Leu	Glu
			260					265					270	
Val	Asn	Glu	Glu	Ser	Thr	Val	Ser	Glu	Ala	Gly	Pro	Asn	Gln	Thr
	275						280					285		
Glu	Val	Pro	Asn	Lys	Ile	Ile	Asn	Arg	Ala	Lys	Glu	Thr	Leu	Lys
	290					295					300			
Asp	Ile	Leu	His	Lys	Gln	Ala	Ser	Gly	Asn	Ile	Val	Tyr	Gly	Val
305					310					315				320
Met	Leu	His	Lys	Lys	Thr	Val	Asn	Gln	Lys	Thr	Thr	Ile	Tyr	Glu
				325					330					335
Gln	Asp	Asp	Arg	Gly	Lys	Met	Asp	Val	Val	Gly	Thr	Gly	Gln	Cys
			340					345					350	
Asn	Ile	Pro	Cys	Glu	Glu	Gly	Asp	Lys	Leu	Gln	Leu	Phe	Cys	Phe
	355						360					365		Arg
Leu	Arg	Lys	Lys	Asn	Gln	Met	Ser	Lys	Leu	Ile	Ser	Glu	Met	His
	370					375					380			Ser
Phe	Ile	Gln	Ile	Lys	Lys	Thr	Asn	Pro	Arg	Asn	Asn	Asp	Pro	Lys
385					390				395					400
Ser	Met	Lys	Leu	Pro	Gln	Glu	Gln	Arg	Gln	Leu	Pro	Tyr	Pro	Ser
			405						410					415
Ala	Ser	Thr	Thr	Phe	Pro	Glu	Ser	His	Leu	Arg	Thr	Pro	Gln	Met
			420					425					430	Pro
Pro	Thr	Thr	Pro	Ser	Ser	Ser	Phe	Phe	Thr	Lys	Lys	Ser	Glu	Asp
	435						440					445		Thr
Ile	Ser	Lys	Met	Asn	Asp	Phe	Met	Arg	Met	Gln	Ile	Leu	Lys	Glu
	450					455				460				Gly
Ser	His	Phe	Pro	Gly	Pro	Phe	Met	Thr	Ser	Ile	Gly	Pro	Ala	Glu
465					470				475					480
His	Pro	His	Thr	Pro	Gln	Met	Pro	Pro	Ser	Thr	Pro	Ser	Ser	Ser
			485					490					495	Phe
Leu	Thr	Thr	Leu	Lys	Pro	Arg	Leu	Lys	Thr	Glu	Pro	Glu	Glu	Val
			500					505					510	Ser
Ile	Glu	Asp	Ser	Ala	Gln	Ser	Asp	Leu	Lys	Glu	Val	Met	Val	Leu
	515						520					525		Asn
Ala	Thr	Glu	Ser	Phe	Val	Tyr	Glu	Pro	Lys	Glu	Gln	Lys	Lys	Met
	530					535				540				Phe
His	Ala	Thr	Val	Ala	Thr	Glu	Asn	Glu	Val	Phe	Arg	Val	Lys	Val
545					550				555					560
Asn	Ile	Asp	Leu	Lys	Glu	Lys	Phe	Thr	Pro	Lys	Lys	Ile	Ile	Ala
			565					570						575
Ala	Asn	Tyr	Val	Cys	Arg	Asn	Gly	Phe	Leu	Glu	Val	Tyr	Pro	Phe
			580					585					590	Thr
Leu	Val	Ala	Asp	Val	Asn	Ala	Asp	Ala	Asn	Met	Glu	Ile	Pro	Lys
	595						600					605		Gly
Leu	Ile	Arg	Ser	Ala	Ser	Val	Thr	Pro	Lys	Ile	Asn	Gln	Leu	Cys
	610						615					620		Ser
Gln	Thr	Lys	Gly	Ser	Phe	Val	Asn	Gly	Val	Phe	Glu	Val	His	Lys
625					630				635					640
Asn	Val	Arg	Gly	Glu	Phe	Thr	Tyr	Tyr	Glu	Ile	Gln	Asp	Asn	Thr
			645					650					655	Gly
Lys	Met	Glu	Val	Val	Val	His	Gly	Arg	Leu	Asn	Thr	Ile	Asn	Cys
			660					665					670	Glu

Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser  
 675 680 685  
 Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val  
 690 695 700  
 Ile Lys Thr Lys Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser  
 705 710 715 720  
 Met Glu Thr Ser Pro Asp Phe Phe Phe  
 725

<210> 68  
 <211> 754  
 <212> PRT  
 <213> Homo Sapiens

<400> 68  
 Met Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro  
 1 5 10 15  
 Pro Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu  
 20 25 30  
 Gln Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe  
 35 40 45  
 Ala Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro  
 50 55 60  
 Asp Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys  
 65 70 75 80  
 Arg Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln  
 85 90 95  
 Asp Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr  
 100 105 110  
 Asp Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln  
 115 120 125  
 Lys Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile  
 130 135 140  
 Pro Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly  
 145 150 155 160  
 Ser Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His  
 165 170 175  
 Thr Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn  
 180 185 190  
 Ile Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His  
 195 200 205  
 Ser Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln  
 210 215 220  
 Pro Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr  
 225 230 235 240  
 Pro Thr Pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro  
 245 250 255  
 Gly Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu  
 260 265 270  
 Ser Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln  
 275 280 285  
 Gln Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys  
 290 295 300  
 His Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala  
 305 310 315 320

Tyr Ala Trp Pro Phe Tyr Lys Pro Val Asp Ala Ser Ala Leu Gly Leu  
 325 330 335  
 His Asp Tyr His Asp Ile Ile Lys His Pro Met Asp Leu Ser Thr Val  
 340 345 350  
 Lys Arg Lys Met Glu Asn Arg Asp Tyr Arg Asp Ala Gln Glu Phe Ala  
 355 360 365  
 Ala Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro  
 370 375 380  
 Asp His Asp Val Val Ala Met Ala Arg Lys Leu Gln Asp Val Phe Glu  
 385 390 395 400  
 Phe Arg Tyr Ala Lys Met Pro Asp Glu Pro Leu Glu Pro Gly Pro Leu  
 405 410 415  
 Pro Val Ser Thr Ala Met Pro Pro Gly Leu Ala Lys Ser Ser Ser Glu  
 420 425 430  
 Ser Ser Ser Glu Glu Ser Ser Ser Glu Ser Ser Ser Glu Glu Glu Glu  
 435 440 445  
 Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Ser Glu Ser Ser Asp  
 450 455 460  
 Ser Glu Glu Glu Arg Ala His Arg Leu Ala Glu Leu Gln Glu Gln Leu  
 465 470 475 480  
 Arg Ala Val His Glu Gln Leu Ala Ala Leu Ser Gln Gly Pro Ile Ser  
 485 490 495  
 Lys Pro Lys Arg Lys Arg Glu Lys Lys Glu Lys Lys Lys Lys Arg Lys  
 500 505 510  
 Ala Glu Lys His Arg Gly Arg Ala Gly Ala Asp Glu Asp Asp Lys Gly  
 515 520 525  
 Pro Arg Ala Pro Arg Pro Pro Gln Pro Lys Lys Ser Lys Lys Ala Ser  
 530 535 540  
 Gly Ser Gly Gly Gly Ser Ala Ala Leu Gly Pro Ser Gly Phe Gly Pro  
 545 550 555 560  
 Ser Gly Gly Ser Gly Thr Lys Leu Pro Lys Lys Ala Thr Lys Thr Ala  
 565 570 575  
 Pro Pro Ala Leu Pro Thr Gly Tyr Asp Ser Glu Glu Glu Glu Glu Ser  
 580 585 590  
 Arg Pro Met Ser Tyr Asp Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn  
 595 600 605  
 Lys Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ala  
 610 615 620  
 Arg Glu Pro Ser Leu Arg Asp Ser Asn Pro Glu Glu Ile Glu Ile Asp  
 625 630 635 640  
 Phe Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val  
 645 650 655  
 Leu Ser Cys Leu Arg Lys Lys Pro Arg Lys Pro Tyr Thr Ile Lys Lys  
 660 665 670  
 Pro Val Gly Lys Thr Lys Glu Glu Leu Ala Leu Glu Lys Lys Arg Glu  
 675 680 685  
 Leu Glu Lys Arg Leu Gln Asp Val Ser Gly Gln Leu Asn Ser Thr Lys  
 690 695 700  
 Lys Pro Pro Lys Lys Ala Asn Glu Lys Thr Glu Ser Ser Ser Ala Gln  
 705 710 715 720  
 Gln Val Ala Val Ser Arg Leu Ser Ala Ser Ser Ser Ser Ser Asp Ser  
 725 730 735  
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Thr Ser Asp Ser Asp  
 740 745 750  
 Ser Gly

<210> 69  
 <211> 210  
 <212> PRT  
 <213> Homo Sapiens

<400> 69  
 Met Asp Asp Glu Glu Glu Thr Tyr Arg Leu Trp Lys Ile Arg Lys Thr  
 1 5 10 15  
 Ile Met Gln Leu Cys His Asp Arg Gly Tyr Leu Val Thr Gln Asp Glu  
 20 25 30  
 Leu Asp Gln Thr Leu Glu Glu Phe Lys Ala Gln Phe Gly Asp Lys Pro  
 35 40 45  
 Ser Glu Gly Arg Pro Arg Arg Thr Asp Leu Thr Val Leu Val Ala His  
 50 55 60  
 Asn Asp Asp Pro Thr Asp Gln Met Phe Val Phe Phe Pro Glu Glu Pro  
 65 70 75 80  
 Lys Val Gly Ile Lys Thr Ile Lys Val Tyr Cys Gln Arg Met Gln Glu  
 85 90 95  
 Glu Asn Ile Thr Arg Ala Leu Ile Val Val Gln Gln Gly Met Thr Pro  
 100 105 110  
 Ser Ala Lys Gln Ser Leu Val Asp Met Ala Pro Lys Tyr Ile Leu Glu  
 115 120 125  
 Gln Phe Leu Gln Gln Glu Leu Ile Asn Ile Thr Glu His Glu Leu  
 130 135 140  
 Val Pro Glu His Val Val Met Thr Lys Glu Glu Val Thr Glu Leu Leu  
 145 150 155 160  
 Ala Arg Tyr Lys Leu Arg Glu Asn Gln Leu Pro Arg Ile Gln Ala Gly  
 165 170 175  
 Asp Pro Val Ala Arg Tyr Phe Gly Ile Lys Arg Gly Gln Val Val Lys  
 180 185 190  
 Ile Ile Arg Pro Ser Glu Thr Ala Gly Arg Tyr Ile Thr Tyr Arg Leu  
 195 200 205  
 Val Gln  
 210

<210> 70  
 <211> 621  
 <212> PRT  
 <213> Homo Sapiens

<400> 70  
 Met Leu Leu Leu Pro Ser Ala Ala Glu Gly Gln Gly Thr Ala Ile Thr  
 1 5 10 15  
 His Ala Leu Thr Ser Ala Ser Ser Val Cys Gln Val Glu Pro Val Gly  
 20 25 30  
 Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Thr  
 35 40 45  
 Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu  
 50 55 60  
 Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp  
 65 70 75 80  
 Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly  
 85 90 95

His Val Arg Tyr Thr Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys  
 100 105 110  
 Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu  
 115 120 125  
 Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala  
 130 135 140  
 Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val  
 145 150 155 160  
 Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp  
 165 170 175  
 Asn Phe Phe Gln Val Phe Ser Pro Val Phe Glu Arg Asn Ser Arg Trp  
 180 185 190  
 Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe  
 195 200 205  
 Glu Asp Val Asp Ala Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp  
 210 215 220  
 Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys  
 225 230 235 240  
 Arg Asp Glu Arg Lys Trp Ile Glu Lys Gln Asn Arg Ala Thr Arg Ala  
 245 250 255  
 Gln Arg Lys Lys Glu Glu Met Asn Arg Ile Arg Thr Leu Val Asp Asn  
 260 265 270  
 Ala Tyr Ser Cys Asp Pro Arg Ile Lys Lys Phe Lys Glu Glu Glu Lys  
 275 280 285  
 Ala Lys Lys Glu Ala Glu Lys Lys Ala Lys Ala Glu Ala Arg Arg Lys  
 290 295 300  
 Glu Gln Glu Ala Lys Glu Lys Gln Arg Gln Ala Glu Leu Glu Ala Val  
 305 310 315 320  
 Arg Leu Ala Lys Glu Lys Glu Glu Glu Glu Val Arg Gln Gln Ala Leu  
 325 330 335  
 Leu Ala Lys Lys Glu Lys Asp Ile Gln Lys Lys Ala Ile Lys Lys Glu  
 340 345 350  
 Arg Gln Lys Leu Arg Asn Ser Cys Lys Ser Trp Asn His Phe Ser Asp  
 355 360 365  
 Asn Glu Ala Asp Arg Val Lys Met Met Glu Glu Val Glu Lys Leu Cys  
 370 375 380  
 Asp Arg Leu Glu Leu Ala Ser Leu Gln Gly Leu Asn Glu Ile Leu Ala  
 385 390 395 400  
 Ser Ser Thr Arg Glu Val Gly Lys Ala Ala Leu Glu Lys Gln Ile Glu  
 405 410 415  
 Glu Val Asn Glu Gln Met Arg Arg Glu Lys Glu Glu Ala Asp Ala Arg  
 420 425 430  
 Met Arg Gln Ala Ser Lys Asn Ala Glu Lys Ser Thr Gly Gly Ser Gly  
 435 440 445  
 Ser Gly Ser Lys Asn Trp Ser Glu Asp Asp Leu Gln Leu Leu Ile Lys  
 450 455 460  
 Ala Val Asn Leu Phe Pro Ala Gly Thr Asn Ser Arg Trp Glu Val Ile  
 465 470 475 480  
 Ala Asn Tyr Met Asn Ile His Ser Ser Ser Gly Val Lys Arg Thr Ala  
 485 490 495  
 Lys Asp Val Ile Ser Lys Ala Lys Ser Leu Gln Lys Leu Asp Pro His  
 500 505 510  
 Gln Lys Asp Asp Ile Asn Lys Lys Ala Phe Asp Lys Phe Lys Lys Glu  
 515 520 525  
 His Gly Val Ala Ser Gln Ala Asp Ser Ala Ala Pro Ser Glu Arg Phe

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      530                      535                      540
Glu Gly Pro Cys Ile Asp Ser Thr Pro Trp Thr Thr Glu Glu Gln Lys
545                      550                      555                      560
Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Thr Pro Glu Arg
      565                      570                      575
Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Asp Cys
      580                      585                      590
Met Arg Arg Tyr Lys Glu Leu Val Glu Met Val Lys Ala Lys Lys Ala
      595                      600                      605
Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Arg Lys
      610                      615                      620

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<210> 71  
 <211> 267  
 <212> PRT  
 <213> Homo Sapiens

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      <400> 71
Met Ala Ser Leu Leu Lys Val Asp Gln Glu Val Lys Leu Lys Val Asp
  1                      5                      10                      15
Ser Phe Arg Glu Arg Ile Thr Ser Lys Ala Glu Asp Leu Val Ala Asn
      20                      25                      30
Phe Phe Pro Lys Lys Leu Leu Glu Leu Asp Ser Phe Leu Lys Glu Pro
      35                      40                      45
Ile Leu Asn Ile His Asp Leu Thr Gln Ile His Ser Asp Met Asn Leu
      50                      55                      60
Pro Val Pro Asp Pro Ile Leu Leu Thr Asn Ser His Asp Gly Leu Asp
65                      70                      75                      80
Gly Pro Thr Tyr Lys Lys Arg Arg Leu Asp Glu Cys Glu Glu Ala Phe
      85                      90                      95
Gln Gly Thr Lys Val Phe Val Met Pro Asn Gly Met Leu Lys Ser Asn
      100                      105                      110
Gln Gln Leu Val Asp Ile Ile Glu Lys Val Lys Pro Glu Ile Arg Leu
      115                      120                      125
Leu Ile Glu Lys Cys Asn Thr Pro Ser Gly Lys Gly Pro His Ile Cys
      130                      135                      140
Phe Asp Leu Gln Val Lys Met Trp Val Gln Leu Leu Ile Pro Arg Ile
145                      150                      155                      160
Glu Asp Gly Asn Asn Phe Gly Val Ser Ile Gln Glu Glu Thr Val Ala
      165                      170                      175
Glu Leu Arg Thr Val Glu Ser Glu Ala Ala Ser Tyr Leu Asp Gln Ile
      180                      185                      190
Ser Arg Tyr Tyr Ile Thr Arg Ala Lys Leu Val Ser Lys Ile Ala Lys
      195                      200                      205
Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu Ile Asp Glu
      210                      215                      220
Lys Glu Tyr Ile Ser Leu Arg Leu Ile Ile Ser Glu Leu Arg Asn Gln
225                      230                      235                      240
Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile Glu Lys Ile Lys
      245                      250                      255
Arg Pro Arg Ser Ser Asn Ala Glu Thr Leu Tyr
      260                      265

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<210> 72  
 <211> 1752



&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 72

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Arg Glu Lys Arg Arg Lys Ser Val Glu Asp Arg Phe Asp Gln Gln
 1           5           10           15
Lys Asn Asp Tyr Asp Gln Leu Gln Lys Ala Arg Gln Cys Glu Lys Glu
          20           25           30
Asn Leu Gly Trp Gln Lys Leu Glu Ser Glu Lys Ala Ile Lys Glu Lys
          35           40           45
Glu Tyr Glu Ile Glu Arg Leu Arg Val Leu Leu Gln Glu Glu Gly Thr
          50           55           60
Arg Lys Arg Glu Tyr Glu Asn Glu Leu Ala Lys Val Arg Asn His Tyr
65           70           75           80
Asn Glu Glu Met Ser Asn Leu Arg Asn Lys Tyr Glu Thr Glu Ile Asn
          85           90           95
Ile Thr Lys Thr Thr Ile Lys Glu Ile Ser Met Gln Lys Glu Asp Asp
          100          105          110
Ser Lys Asn Leu Arg Asn Gln Leu Asp Arg Leu Ser Arg Glu Asn Arg
          115          120          125
Asp Leu Lys Asp Glu Ile Val Arg Leu Asn Asp Ser Ile Leu Gln Ala
          130          135          140
Thr Glu Gln Arg Arg Arg Ala Glu Glu Asn Ala Leu Gln Gln Lys Ala
          145          150          155          160
Cys Gly Ser Glu Ile Met Gln Lys Lys Gln His Leu Glu Ile Glu Leu
          165          170          175
Lys Gln Val Met Gln Gln Arg Ser Glu Asp Asn Ala Arg His Lys Gln
          180          185          190
Ser Leu Glu Glu Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile
          195          200          205
Glu Arg Leu Lys Ala Glu Phe Gln Glu Glu Ala Lys Arg Arg Trp Glu
          210          215          220
Tyr Glu Asn Glu Leu Ser Lys Val Arg Asn Asn Tyr Asp Glu Glu Ile
          225          230          235          240
Ile Ser Leu Lys Asn Gln Phe Glu Thr Glu Ile Asn Ile Thr Lys Thr
          245          250          255
Thr Ile His Gln Leu Thr Met Gln Lys Glu Glu Asp Thr Ser Gly Tyr
          260          265          270
Arg Ala Gln Ile Asp Asn Leu Thr Arg Glu Asn Arg Ser Leu Ser Glu
          275          280          285
Glu Ile Lys Arg Leu Lys Asn Thr Leu Thr Gln Thr Thr Glu Asn Leu
          290          295          300
Arg Arg Val Glu Glu Asp Ile Gln Gln Gln Lys Ala Thr Gly Ser Glu
          305          310          315          320
Val Ser Gln Arg Lys Gln Gln Leu Glu Val Glu Leu Arg Gln Val Thr
          325          330          335
Gln Met Arg Thr Glu Glu Ser Val Arg Tyr Lys Gln Ser Leu Asp Asp
          340          345          350
Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile Glu Arg Leu Lys
          355          360          365
Gln Leu Ile Asp Lys Glu Thr Asn Asp Arg Lys Cys Leu Glu Asp Glu
          370          375          380
Asn Ala Arg Leu Gln Arg Val Gln Tyr Asp Leu Gln Lys Ala Asn Ser
          385          390          395          400
Ser Ala Thr Glu Thr Ile Asn Lys Leu Lys Val Gln Glu Gln Glu Leu

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Phe Asp Gly Leu Arg Lys Lys Val Thr Ala Met Gln Leu Tyr Glu Cys  
 850 855 860  
 Gln Leu Ile Asp Lys Thr Leu Asp Lys Leu Leu Lys Gly Lys Lys  
 865 870 875 880  
 Ser Val Glu Glu Val Ala Ser Glu Ile Gln Pro Phe Leu Arg Gly Ala  
 885 890 895  
 Gly Ser Ile Ala Gly Ala Ser Ala Ser Pro Lys Glu Lys Tyr Ser Leu  
 900 905 910  
 Val Glu Ala Lys Arg Lys Lys Leu Ile Ser Pro Glu Ser Thr Val Met  
 915 920 925  
 Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Ile Ile Asp Pro His Arg  
 930 935 940  
 Asn Glu Lys Leu Thr Val Asp Ser Ala Ile Ala Arg Asp Leu Ile Asp  
 945 950 955 960  
 Phe Asp Asp Arg Gln Gln Ile Tyr Ala Ala Glu Lys Ala Ile Thr Gly  
 965 970 975  
 Phe Asp Asp Pro Phe Ser Gly Lys Thr Val Ser Val Ser Glu Ala Ile  
 980 985 990  
 Lys Lys Asn Leu Ile Asp Arg Glu Thr Gly Met Arg Leu Leu Glu Ala  
 995 1000 1005  
 Gln Ile Ala Ser Gly Gly Val Val Asp Pro Val Asn Ser Val Phe Leu  
 1010 1015 1020  
 Pro Lys Asp Val Ala Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr  
 1025 1030 1035 104  
 Arg Ser Leu Asn Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro  
 1045 1050 1055  
 Val Thr Lys Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg  
 1060 1065 1070  
 Ile Glu Pro His Thr Gly Leu Leu Leu Leu Ser Val Gln Lys Arg Ser  
 1075 1080 1085  
 Met Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val  
 1090 1095 1100  
 Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser Gly  
 1105 1110 1115 112  
 Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe Leu Gln  
 1125 1130 1135  
 Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr Lys Gln Lys  
 1140 1145 1150  
 Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val Arg Pro Gly Thr  
 1155 1160 1165  
 Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Ile Val Asp  
 1170 1175 1180  
 Pro Val Ser Asn Leu Arg Leu Pro Val Glu Glu Ala Tyr Lys Arg Gly  
 1185 1190 1195 120  
 Leu Val Gly Ile Glu Phe Lys Glu Lys Leu Leu Ser Ala Glu Arg Ala  
 1205 1210 1215  
 Val Thr Gly Tyr Asn Asp Pro Glu Thr Gly Asn Ile Ile Ser Leu Phe  
 1220 1225 1230  
 Gln Ala Met Asn Lys Glu Leu Ile Glu Lys Gly His Gly Ile Arg Leu  
 1235 1240 1245  
 Leu Glu Ala Gln Ile Ala Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser  
 1250 1255 1260  
 His Arg Leu Pro Val Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu  
 1265 1270 1275 128  
 Glu Leu Ser Glu Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe

	1285		1290		1295
Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu					
	1300		1305		1310
Arg Cys Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys					
	1315		1320		1325
Glu Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys					
	1330		1335		1340
Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser Val					
	1345		1350		1355
Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe Lys Glu					
	1365		1370		1375
Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile Thr Gly Ser					
	1380		1385		1390
Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys Thr Gly Ser Gln					
	1395		1400		1405
Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu Val Asp Arg Lys Phe					
	1410		1415		1420
Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser Leu Thr Gln Phe Ala Asp					
	1425		1430		1435
Met Ile Ser Leu Lys Asn Gly Val Gly Thr Ser Ser Ser Met Gly Ser					
	1445		1450		1455
Gly Val Ser Asp Asp Val Phe Ser Ser Ser Arg His Glu Ser Val Ser					
	1460		1465		1470
Lys Ile Ser Thr Ile Ser Ser Val Arg Asn Leu Thr Ile Arg Ser Ser					
	1475		1480		1485
Ser Phe Ser Asp Thr Leu Glu Glu Ser Ser Pro Ile Ala Ala Ile Phe					
	1490		1495		1500
Asp Thr Glu Asn Leu Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg					
	1505		1510		1515
Gly Ile Val Asp Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala					
	1525		1530		1535
Cys Thr Gly Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu					
	1540		1545		1550
Gln Asp Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser					
	1555		1560		1565
Val Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly					
	1570		1575		1580
Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu Pro					
	1585		1590		1595
Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr Gly Gly					
	1605		1610		1615
Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu Glu Ala Ile					
	1620		1625		1630
Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg Leu Gln Asp Thr					
	1635		1640		1645
Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys Thr Lys Leu Lys Ile					
	1650		1655		1660
Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met Val Glu Asp Ile Thr Gly					
	1665		1670		1675
Leu Arg Leu Leu Glu Ala Ala Ser Val Ser Ser Lys Gly Leu Pro Ser					
	1685		1690		1695
Pro Tyr Asn Met Ser Ser Ala Pro Gly Ser Arg Ser Gly Ser Arg Ser					
	1700		1705		1710
Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Arg					
	1715		1720		1725

Gly Ser Phe Asp Ala Thr Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser  
 1730 1735 1740  
 Phe Ser Ser Ser Ser Ile Gly His  
 1745 1750

<210> 73  
 <211> 1978  
 <212> PRT  
 <213> Homo Sapiens

<400> 73  
 Met Ser Arg Pro Arg Phe Asn Pro Arg Gly Asp Phe Pro Leu Gln Arg  
 1 5 10 15  
 Pro Arg Ala Pro Asn Pro Ser Gly Met Arg Pro Pro Gly Pro Phe Met  
 20 25 30  
 Arg Pro Gly Ser Met Gly Leu Pro Arg Phe Tyr Pro Ala Gly Arg Ala  
 35 40 45  
 Arg Gly Ile Pro His Arg Phe Ala Gly Leu Glu Ser Tyr Gln Asn Met  
 50 55 60  
 Gly Pro Gln Arg Met Asn Val Gln Val Thr Gln His Arg Thr Asp Pro  
 65 70 75 80  
 Arg Leu Thr Lys Glu Lys Leu Asp Phe His Glu Ala Gln Gln Lys Lys  
 85 90 95  
 Gly Lys Pro His Gly Ser Arg Trp Asp Glu Pro His Ile Ser Ala  
 100 105 110  
 Ser Val Ala Val Lys Gln Ser Ser Val Thr Gln Val Thr Glu Gln Ser  
 115 120 125  
 Pro Lys Val Gln Ser Arg Tyr Thr Lys Glu Ser Ala Ser Ser Ile Leu  
 130 135 140  
 Ala Ser Phe Gly Leu Ser Asn Glu Asp Leu Glu Glu Leu Ser Arg Tyr  
 145 150 155 160  
 Pro Asp Glu Gln Leu Thr Pro Glu Asn Met Pro Leu Ile Leu Arg Asp  
 165 170 175  
 Ile Arg Met Arg Lys Met Gly Arg Arg Leu Pro Asn Leu Pro Ser Gln  
 180 185 190  
 Ser Arg Asn Lys Glu Thr Leu Gly Ser Glu Ala Val Ser Ser Asn Val  
 195 200 205  
 Ile Asp Tyr Gly His Ala Ser Lys Tyr Gly Tyr Thr Glu Asp Pro Leu  
 210 215 220  
 Glu Val Arg Ile Tyr Asp Pro Glu Ile Pro Thr Asp Glu Val Glu Asn  
 225 230 235 240  
 Glu Phe Gln Ser Gln Asn Ile Ser Ala Ser Val Pro Asn Pro Asn  
 245 250 255  
 Val Ile Cys Asn Ser Met Phe Pro Val Glu Asp Val Phe Arg Gln Met  
 260 265 270  
 Asp Phe Pro Gly Glu Ser Ser Asn Asn Arg Ser Phe Phe Ser Val Glu  
 275 280 285  
 Ser Gly Thr Lys Met Ser Gly Leu His Ile Ser Gly Gly Gln Ser Val  
 290 295 300  
 Leu Glu Pro Ile Lys Ser Val Asn Gln Ser Ile Asn Gln Thr Val Ser  
 305 310 315 320  
 Gln Thr Met Ser Gln Ser Leu Ile Pro Pro Ser Met Asn Gln Gln Pro  
 325 330 335  
 Phe Ser Ser Glu Leu Ile Ser Ser Val Ser Gln Gln Glu Arg Ile Pro  
 340 345 350

His Glu Pro Val Ile Asn Ser Ser Asn Val His Val Gly Ser Arg Gly  
 355 360 365  
 Ser Lys Lys Asn Tyr Gln Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro  
 370 375 380  
 Phe Gly Ile Val Lys Ala Ser Trp Leu Pro Lys Phe Ser His Ala Asp  
 385 390 395 400  
 Ala Gln Lys Met Lys Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr  
 405 410 415  
 Tyr Ala Ala Ser Pro Arg Ile Phe Pro His Leu Cys Ser Leu Cys Asn  
 420 425 430  
 Val Glu Cys Ser His Leu Lys Asp Trp Ile Gln His Gln Asn Thr Ser  
 435 440 445  
 Thr His Ile Glu Ser Cys Arg Gln Leu Arg Gln Gln Tyr Pro Asp Trp  
 450 455 460  
 Asn Pro Glu Ile Leu Pro Ser Arg Arg Asn Glu Gly Asn Arg Lys Glu  
 465 470 475 480  
 Asn Glu Thr Pro Arg Arg Arg Ser His Ser Pro Ser Pro Arg Arg Ser  
 485 490 495  
 Arg Arg Ser Ser Ser Ser His Arg Phe Arg Arg Ser Arg Ser Pro Met  
 500 505 510  
 His Tyr Met Tyr Arg Pro Arg Ser Arg Ser Pro Arg Ile Cys His Arg  
 515 520 525  
 Phe Ile Ser Arg Tyr Arg Ser Arg Ser Arg Ser Arg Ser Pro Tyr Arg  
 530 535 540  
 Ile Arg Asn Pro Phe Arg Gly Ser Pro Lys Cys Phe Arg Ser Val Ser  
 545 550 555 560  
 Pro Glu Arg Met Ser Arg Arg Ser Val Arg Ser Ser Asp Arg Lys Lys  
 565 570 575  
 Ala Leu Glu Asp Val Val Gln Arg Ser Gly His Gly Thr Glu Phe Asn  
 580 585 590  
 Lys Gln Lys His Leu Glu Ala Ala Asp Lys Gly His Ser Pro Ala Gln  
 595 600 605  
 Lys Pro Lys Thr Ser Ser Gly Thr Lys Pro Ser Val Lys Pro Thr Ser  
 610 615 620  
 Ala Thr Lys Ser Asp Ser Asn Leu Gly Gly His Ser Ile Arg Cys Lys  
 625 630 635 640  
 Ser Lys Asn Leu Glu Asp Asp Thr Leu Ser Glu Cys Lys Gln Val Ser  
 645 650 655  
 Asp Lys Ala Val Ser Leu Gln Arg Lys Leu Arg Lys Glu Gln Ser Leu  
 660 665 670  
 His Tyr Gly Ser Val Leu Leu Ile Thr Glu Leu Pro Glu Asp Gly Cys  
 675 680 685  
 Thr Glu Glu Asp Val Arg Lys Leu Phe Gln Pro Phe Gly Lys Val Asn  
 690 695 700  
 Asp Val Leu Ile Val Pro Tyr Arg Lys Glu Ala Tyr Leu Glu Met Glu  
 705 710 715 720  
 Phe Lys Glu Ala Ile Thr Ala Ile Met Lys Tyr Ile Glu Thr Thr Pro  
 725 730 735  
 Leu Thr Ile Lys Gly Lys Ser Val Lys Ile Cys Val Pro Gly Lys Lys  
 740 745 750  
 Lys Ala Gln Asn Lys Glu Val Lys Lys Lys Thr Leu Glu Ser Lys Lys  
 755 760 765  
 Val Ser Ala Ser Thr Leu Lys Arg Asp Ala Asp Ala Ser Lys Ala Val  
 770 775 780  
 Glu Ile Val Thr Ser Thr Ser Ala Ala Lys Thr Gly Gln Ala Lys Ala

785		790		795		800
Cys Val Ala Lys Val Asn Lys Ser Thr Gly Lys Ser Ala Ser Ser Val						
	805			810		815
Lys Ser Val Val Thr Val Ala Val Lys Gly Asn Lys Ala Ser Ile Lys						
	820			825		830
Thr Ala Lys Ser Gly Gly Lys Lys Ser Leu Glu Ala Lys Lys Thr Gly						
	835			840		845
Asn Val Lys Asn Lys Asp Ser Asn Lys Pro Val Thr Ile Pro Glu Asn						
	850			855		860
Ser Glu Ile Lys Thr Ser Ile Glu Val Lys Ala Thr Glu Asn Cys Ala						
865		870		875		880
Lys Glu Ala Ile Ser Asp Ala Ala Leu Glu Ala Thr Glu Asn Glu Pro						
	885			890		895
Leu Asn Lys Glu Thr Glu Glu Met Cys Val Met Leu Val Ser Asn Leu						
	900			905		910
Pro Asn Lys Gly Tyr Ser Val Glu Glu Val Tyr Asp Leu Ala Lys Pro						
	915			920		925
Phe Gly Gly Leu Lys Asp Ile Leu Ile Leu Ser Ser His Lys Lys Ala						
930		935		940		
Tyr Ile Glu Ile Asn Arg Lys Ala Ala Glu Ser Met Val Lys Phe Tyr						
945		950		955		960
Thr Cys Phe Pro Val Leu Met Asp Gly Asn Gln Leu Ser Ile Ser Met						
	965			970		975
Ala Pro Glu Asn Met Asn Ile Lys Asp Glu Glu Ala Ile Phe Ile Thr						
	980			985		990
Leu Val Lys Glu Asn Asp Pro Glu Ala Asn Ile Asp Thr Ile Tyr Asp						
	995			1000		1005
Arg Phe Val His Leu Asp Asn Leu Pro Glu Asp Gly Leu Gln Cys Val						
1010		1015		1020		
Leu Cys Val Gly Leu Gln Phe Gly Lys Val Asp His His Val Phe Ile						
1025		1030		1035		104
Ser Asn Arg Asn Lys Ala Ile Leu Gln Leu Asp Ser Pro Glu Ser Ala						
	1045			1050		1055
Gln Ser Met Tyr Ser Phe Leu Lys Gln Asn Pro Gln Asn Ile Gly Asp						
	1060			1065		1070
His Met Leu Thr Cys Ser Leu Ser Pro Lys Ile Asp Leu Pro Glu Val						
	1075			1080		1085
Gln Ile Glu His Asp Pro Glu Leu Glu Lys Glu Ser Pro Gly Leu Lys						
	1090			1095		1100
Asn Ser Pro Ile Asp Glu Ser Glu Val Gln Thr Ala Thr Asp Ser Pro						
1105		1110		1115		112
Ser Val Lys Pro Asn Glu Leu Glu Glu Glu Ser Thr Pro Ser Ile Gln						
	1125			1130		1135
Thr Glu Thr Leu Val Gln Gln Glu Glu Pro Cys Glu Glu Glu Ala Glu						
	1140			1145		1150
Lys Ala Thr Cys Asp Ser Asp Phe Ala Val Glu Thr Leu Glu Leu Glu						
	1155			1160		1165
Thr Gln Gly Glu Glu Val Lys Glu Glu Ile Pro Leu Val Ala Ser Ala						
	1170			1175		1180
Ser Val Ser Ile Glu Gln Phe Thr Glu Asn Ala Glu Glu Cys Ala Leu						
1185		1190		1195		120
Asn Gln Gln Met Phe Asn Ser Asp Leu Glu Lys Lys Gly Ala Glu Ile						
	1205			1210		1215
Ile Asn Pro Lys Thr Ala Leu Leu Pro Ser Asp Ser Val Phe Ala Glu						
	1220			1225		1230

Glu Arg Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu  
 1235 1240 1245  
 Asp Phe Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu  
 1250 1255 1260  
 Val Glu Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile  
 1265 1270 1275 128  
 Val Thr Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp  
 1285 1290 1295  
 Lys Lys Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu  
 1300 1305 1310  
 Lys Glu Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr  
 1315 1320 1325  
 Glu Lys Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu  
 1330 1335 1340  
 Lys Met Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys  
 1345 1350 1355 136  
 Ala Tyr Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr  
 1365 1370 1375  
 Ser Lys Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Ser Lys Pro  
 1380 1385 1390  
 Ser Ile Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val  
 1395 1400 1405  
 Ser Lys Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp  
 1410 1415 1420  
 Gln Ile Asn Ala Glu Lys Lys Leu Ser Ala Lys Glu Phe Gly Leu Leu  
 1425 1430 1435 144  
 Lys Pro Thr Ser Ala Arg Ser Gly Leu Ala Glu Ser Ser Ser Lys Phe  
 1445 1450 1455  
 Lys Pro Thr Gln Ser Ser Leu Thr Arg Gly Gly Ser Gly Arg Ile Ser  
 1460 1465 1470  
 Ala Leu Gln Gly Lys Leu Ser Lys Leu Asp Tyr Arg Asp Ile Thr Lys  
 1475 1480 1485  
 Gln Ser Gln Glu Thr Glu Ala Arg Pro Ser Ile Met Lys Arg Asp Asp  
 1490 1495 1500  
 Ser Asn Asn Lys Thr Leu Ala Glu Gln Asn Thr Lys Asn Pro Lys Ser  
 1505 1510 1515 152  
 Thr Thr Gly Arg Ser Ser Lys Ser Lys Glu Glu Pro Leu Phe Pro Phe  
 1525 1530 1535  
 Asn Leu Asp Glu Phe Val Thr Val Asp Glu Val Ile Glu Glu Val Asn  
 1540 1545 1550  
 Pro Ser Gln Ala Lys Gln Asn Pro Leu Lys Gly Lys Arg Lys Glu Thr  
 1555 1560 1565  
 Leu Lys Asn Val Pro Phe Ser Glu Leu Asn Leu Lys Lys Lys Gly  
 1570 1575 1580  
 Lys Thr Ser Thr Pro Arg Gly Val Glu Gly Glu Leu Ser Phe Val Thr  
 1585 1590 1595 160  
 Leu Asp Glu Ile Gly Glu Glu Glu Asp Ala Ala Ala His Leu Ala Gln  
 1605 1610 1615  
 Ala Leu Val Thr Val Asp Glu Val Ile Asp Glu Glu Glu Leu Asn Met  
 1620 1625 1630  
 Glu Glu Met Val Lys Asn Ser Asn Ser Leu Phe Thr Leu Asp Glu Leu  
 1635 1640 1645  
 Ile Asp Gln Asp Asp Cys Ile Ser His Ser Glu Pro Lys Asp Val Thr  
 1650 1655 1660  
 Val Leu Ser Val Ala Glu Glu Gln Asp Leu Leu Lys Gln Glu Arg Leu



1665                      1670                      1675                      168  
 Val Thr Val Asp Glu Ile Gly Glu Val Glu Glu Leu Pro Leu Asn Glu  
                                  1685                      1690                      1695  
 Ser Ala Asp Ile Thr Phe Ala Thr Leu Asn Thr Lys Gly Asn Glu Gly  
                                  1700                      1705                      1710  
 Asp Ile Val Arg Asp Ser Ile Gly Phe Ile Ser Ser Gln Val Pro Glu  
                                  1715                      1720                      1725  
 Asp Pro Ser Thr Leu Val Thr Val Asp Glu Ile Gln Asp Asp Ser Ser  
                                  1730                      1735                      1740  
 Asp Leu His Leu Val Thr Leu Asp Glu Val Thr Glu Glu Asp Glu Asp  
 1745                                   1750                                   1755                                   176  
 Ser Leu Ala Asp Phe Asn Asn Leu Lys Glu Glu Leu Asn Phe Val Thr  
                                  1765                                   1770                                   1775  
 Val Asp Glu Val Gly Glu Glu Glu Asp Gly Asp Asn Asp Leu Lys Val  
                                  1780                                   1785                                   1790  
 Glu Leu Ala Gln Ser Lys Asn Asp His Pro Thr Asp Lys Lys Gly Asn  
                                  1795                                   1800                                   1805  
 Arg Lys Lys Arg Ala Val Asp Thr Lys Lys Thr Lys Leu Glu Ser Leu  
                                  1810                                   1815                                   1820  
 Ser Gln Val Gly Pro Val Asn Glu Asn Val Met Glu Glu Asp Leu Lys  
 1825                                   1830                                   1835                                   184  
 Thr Met Ile Glu Arg His Leu Thr Ala Lys Thr Pro Thr Lys Arg Val  
                                  1845                                   1850                                   1855  
 Arg Ile Gly Lys Thr Leu Pro Ser Glu Lys Ala Val Val Thr Glu Pro  
                                  1860                                   1865                                   1870  
 Ala Lys Gly Glu Glu Ala Phe Gln Met Ser Glu Val Asp Glu Glu Ser  
                                  1875                                   1880                                   1885  
 Gly Leu Lys Asp Ser Glu Pro Glu Arg Lys Arg Lys Lys Thr Glu Asp  
                                  1890                                   1895                                   1900  
 Ser Ser Ser Gly Lys Ser Val Ala Ser Asp Val Pro Glu Glu Leu Asp  
 1905                                   1910                                   1915                                   192  
 Phe Leu Val Pro Lys Ala Gly Phe Phe Cys Pro Ile Cys Ser Leu Phe  
                                  1925                                   1930                                   1935  
 Tyr Ser Gly Glu Lys Ala Met Thr Asn His Cys Lys Ser Thr Arg His  
                                  1940                                   1945                                   1950  
 Lys Gln Asn Thr Glu Lys Phe Met Ala Lys Gln Arg Lys Glu Lys Glu  
                                  1955                                   1960                                   1965  
 Gln Asn Glu Ala Glu Glu Arg Ser Ser Arg  
                                  1970                                   1975

&lt;210&gt; 74

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 74

Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala  
 1                                      5                                      10                                      15  
 Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe  
                                          20                                           25                                           30  
 Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro His Phe Ile Ala  
                                          35                                           40                                           45  
 Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala  
                                          50                                           55                                           60  
 Ala Ser Pro Arg Gly Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly

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65          70          75          80
Pro Glu Tyr Trp Asp Arg Glu Thr Gln Lys Tyr Lys Arg Gln Ala Gln
      85          90          95
Thr Asp Arg Val Ser Leu Arg Asn Leu Arg Gly Tyr Tyr Asn Gln Ser
      100          105          110
Glu Ala Gly Ser His Ile Ile Gln Arg Met Tyr Gly Cys Asp Val Gly
      115          120          125
Pro Asp Gly Arg Leu Leu Arg Gly Tyr Asp Gln Tyr Ala Tyr Asp Gly
      130          135          140
Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
145          150          155          160
Asp Thr Ala Ala Gln Ile Thr Gln Arg Lys Trp Glu Ala Ala Arg Glu
      165          170          175
Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Leu Cys Val Glu Trp Leu
      180          185          190
Arg Arg Tyr Leu Lys Asn Gly Lys Glu Thr Leu Gln Arg Ala Glu His
      195          200          205
Pro Lys Thr His Val Thr His His Pro Val Ser Asp His Glu Ala Thr
      210          215          220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
225          230          235          240
Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
      245          250          255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
      260          265          270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
      275          280          285
Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
      290          295          300
Thr Ile Pro Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val
305          310          315          320
Leu Ala Val Leu Gly Ala Val Val Ala Val Val Met Cys Arg Arg Lys
      325          330          335
Ser Ser Gly Gly Lys Gly Gly Ser Cys Ser Gln Ala Ala Ser Ser Asn
      340          345          350
Ser Ala Gln Gly Ser Asp Glu Ser Leu Ile Ala Cys Lys Ala
      355          360          365

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<210> 75  
 <211> 240  
 <212> PRT  
 <213> Homo Sapiens

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<400> 75
Met Gly Leu Glu Leu Tyr Leu Asp Leu Leu Ser Gln Pro Cys Arg Ala
1          5          10          15
Val Tyr Ile Phe Ala Lys Lys Asn Asp Ile Pro Phe Glu Leu Arg Ile
      20          25          30
Val Asp Leu Ile Lys Gly Gln His Leu Ser Asp Ala Phe Ala Gln Val
      35          40          45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
      50          55          60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65          70          75          80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp

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				85						90						95	
Glu Tyr Leu Ala Trp Gln His Thr								Thr Leu Arg Arg Ser Cys Leu Arg									
			100					105					110				
Ala Leu Trp His Lys Val Met Phe Pro Val Phe Leu Gly Gly Pro Val								120				125					
			115														
Ser Pro Gln Thr Leu Ala Ala Thr Leu Ala Glu Leu Asp Val Thr Leu																	
			130				135					140					
Gln Leu Leu Glu Asp Lys Phe Leu Gln Asn Lys Ala Phe Leu Thr Gly																	
145					150					155					160		
Pro His Ile Ser Leu Ala Asp Leu Val Ala Ile Thr Glu Leu Met His																	
			165					170						175			
Pro Val Gly Ala Gly Cys Gln Val Phe Glu Gly Arg Pro Lys Leu Ala								185					190				
			180														
Thr Trp Arg Gln Arg Val Glu Ala Val Gly Glu Asp Leu Phe Gln							200					205					
			195														
Glu Ala His Glu Val Ile Leu Lys Ala Lys Asp Phe Pro Pro Ala Asp						215					220						
			210														
Pro Thr Ile Lys Gln Lys Leu Met Pro Trp Val Leu Ala Met Ile Arg																	
225				230						235					240		

<210> 76

<211> 953

<212> PRT

<213> Homo Sapiens

<400> 76

Met	Ile	Thr	Ser	Ala	Ala	Gly	Ile	Ile	Ser	Leu	Leu	Asp	Glu	Asp	Glu
1				5					10					15	
Pro	Gln	Leu	Lys	Glu	Phe	Ala	Leu	His	Lys	Leu	Asn	Ala	Val	Val	Asn
			20					25					30		
Asp	Phe	Trp	Ala	Glu	Ile	Ser	Glu	Ser	Val	Asp	Lys	Ile	Glu	Val	Leu
		35					40					45			
Tyr	Glu	Asp	Glu	Gly	Phe	Arg	Ser	Arg	Gln	Phe	Ala	Ala	Leu	Val	Ala
	50					55				60					
Ser	Lys	Val	Phe	Tyr	His	Leu	Gly	Ala	Phe	Glu	Glu	Ser	Leu	Asn	Tyr
65					70					75				80	
Ala	Leu	Gly	Ala	Arg	Asp	Leu	Phe	Asn	Val	Asn	Asp	Asn	Ser	Glu	Tyr
				85					90					95	
Val	Glu	Thr	Ile	Ile	Ala	Lys	Cys	Ile	Asp	His	Tyr	Thr	Lys	Gln	Cys
			100					105					110		
Val	Glu	Asn	Ala	Asp	Leu	Pro	Glu	Gly	Glu	Lys	Lys	Pro	Ile	Asp	Gln
		115					120					125			
Arg	Leu	Glu	Gly	Ile	Val	Asn	Lys	Met	Phe	Gln	Arg	Cys	Leu	Asp	Asp
	130					135				140					
His	Lys	Tyr	Lys	Gln	Ala	Ile	Gly	Ile	Ala	Leu	Glu	Thr	Arg	Arg	Leu
145				150						155					160
Asp	Val	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Asn	Asp	Val	Pro	Gly	Met
				165					170					175	
Leu	Ala	Tyr	Ser	Leu	Lys	Leu	Cys	Met	Ser	Leu	Met	Gln	Asn	Lys	Gln
			180					185					190		
Phe	Arg	Asn	Lys	Val	Leu	Arg	Val	Leu	Val	Lys	Ile	Tyr	Met	Asn	Leu
		195					200					205			
Glu	Lys	Pro	Asp	Phe	Ile	Asn	Val	Cys	Gln	Cys	Leu	Ile	Phe	Leu	Asp
	210					215					220				
Asp	Pro	Gln	Ala	Val	Ser	Asp	Ile	Leu	Glu	Lys	Leu	Val	Lys	Glu	Asp

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225          230          235          240
Asn Leu Leu Met Ala Tyr Gln Ile Cys Phe Asp Leu Tyr Glu Ser Ala
          245          250          255
Ser Gln Gln Phe Leu Ser Ser Val Ile Gln Asn Leu Arg Thr Val Gly
          260          265          270
Thr Pro Ile Ala Ser Val Pro Gly Ser Thr Asn Thr Gly Thr Val Pro
          275          280          285
Gly Ser Glu Lys Asp Ser Asp Ser Met Glu Thr Glu Glu Lys Thr Ser
          290          295          300
Ser Ala Phe Val Gly Lys Thr Pro Glu Ala Ser Pro Glu Pro Lys Asp
305          310          315          320
Gln Thr Leu Lys Met Ile Lys Ile Leu Ser Gly Glu Met Ala Ile Glu
          325          330          335
Leu His Leu Gln Phe Leu Ile Arg Asn Asn Asn Thr Asp Leu Met Ile
          340          345          350
Leu Lys Asn Thr Lys Asp Ala Val Arg Asn Ser Val Cys His Thr Ala
          355          360          365
Thr Val Ile Ala Asn Ser Phe Met His Cys Gly Thr Thr Ser Asp Gln
          370          375          380
Phe Leu Arg Asp Asn Leu Glu Trp Leu Ala Arg Ala Thr Asn Trp Ala
385          390          395          400
Lys Phe Thr Ala Thr Ala Ser Leu Gly Val Ile His Lys Gly His Glu
          405          410          415
Lys Glu Ala Leu Gln Leu Met Ala Thr Tyr Leu Pro Lys Asp Thr Ser
          420          425          430
Pro Gly Ser Ala Tyr Gln Glu Gly Gly Gly Leu Tyr Ala Leu Gly Leu
          435          440          445
Ile His Ala Asn His Gly Gly Asp Ile Ile Asp Tyr Leu Leu Asn Gln
          450          455          460
Leu Lys Asn Ala Ser Asn Asp Ile Val Arg His Gly Gly Ser Leu Gly
465          470          475          480
Leu Gly Leu Ala Ala Met Gly Thr Ala Arg Gln Asp Val Tyr Asp Leu
          485          490          495
Leu Lys Thr Asn Leu Tyr Gln Asp Asp Ala Val Thr Gly Glu Ala Ala
          500          505          510
Gly Leu Ala Leu Gly Leu Val Met Leu Gly Ser Lys Asn Ala Gln Ala
          515          520          525
Ile Glu Asp Met Val Gly Tyr Ala Gln Glu Thr Gln His Glu Lys Ile
          530          535          540
Leu Arg Gly Leu Ala Val Gly Ile Ala Leu Val Met Tyr Gly Arg Met
545          550          555          560
Glu Glu Ala Asp Ala Leu Ile Glu Ser Leu Cys Arg Asp Lys Asp Pro
          565          570          575
Ile Leu Arg Arg Ser Gly Met Tyr Thr Val Ala Met Ala Tyr Cys Gly
          580          585          590
Ser Gly Asn Asn Lys Ala Ile Arg Arg Leu Leu His Val Ala Val Ser
          595          600          605
Asp Val Asn Asp Asp Val Arg Ser Ala Ala Val Glu Ser Leu Gly Phe
          610          615          620
Ile Leu Phe Arg Thr Pro Glu Gln Cys Pro Ser Val Val Ser Leu Leu
625          630          635          640
Ser Glu Ser Tyr Asn Pro His Val Arg Tyr Gly Ala Ala Met Ala Leu
          645          650          655
Gly Ile Cys Cys Ala Gly Thr Gly Asn Lys Glu Ala Ile Asn Leu Leu
          660          665          670

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Glu Pro Met Thr Asn Asp Pro Val Asn Tyr Val Arg Gln Gly Ala Leu  
 675 680 685  
 Ile Ala Ser Ala Leu Ile Met Ile Gln Gln Thr Glu Ile Thr Cys Pro  
 690 695 700  
 Lys Val Asn Gln Phe Arg Gln Leu Tyr Ser Lys Val Ile Asn Asp Lys  
 705 710 715 720  
 His Asp Asp Val Met Ala Lys Phe Gly Ala Ile Leu Ala Gln Gly Ile  
 725 730 735  
 Leu Asp Ala Gly Gly His Asn Val Thr Ile Ser Leu Gln Ser Arg Thr  
 740 745 750  
 Gly His Thr His Met Pro Ser Val Val Gly Val Leu Val Phe Thr Gln  
 755 760 765  
 Phe Trp Phe Trp Phe Pro Leu Ser His Phe Leu Ser Leu Ala Tyr Thr  
 770 775 780  
 Pro Thr Cys Val Ile Gly Leu Asn Lys Asp Leu Lys Met Pro Lys Val  
 785 790 795 800  
 Gln Tyr Lys Ser Asn Cys Lys Pro Ser Thr Phe Ala Tyr Pro Ala Pro  
 805 810 815  
 Leu Glu Val Pro Lys Glu Lys Glu Lys Glu Lys Val Ser Thr Ala Val  
 820 825 830  
 Leu Ser Ile Thr Ala Lys Ala Lys Lys Glu Lys Glu Lys Glu Lys  
 835 840 845  
 Lys Glu Glu Glu Lys Met Glu Val Asp Glu Ala Glu Lys Lys Glu Glu  
 850 855 860  
 Lys Glu Lys Lys Lys Glu Pro Glu Pro Asn Phe Gln Leu Leu Asp Asn  
 865 870 875 880  
 Pro Ala Arg Val Met Pro Ala Gln Leu Lys Val Leu Thr Met Pro Glu  
 885 890 895  
 Thr Cys Arg Tyr Gln Pro Phe Lys Pro Leu Ser Ile Gly Gly Ile Ile  
 900 905 910  
 Ile Leu Lys Asp Thr Ser Glu Asp Ile Glu Glu Leu Val Glu Pro Val  
 915 920 925  
 Ala Ala His Gly Pro Lys Ile Glu Glu Glu Glu Gln Glu Pro Glu Pro  
 930 935 940  
 Pro Glu Pro Phe Glu Tyr Ile Asp Asp  
 945 950

&lt;210&gt; 77

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 77

Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg  
 1 5 10 15  
 Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala  
 20 25 30  
 Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln  
 35 40 45  
 Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn  
 50 55 60  
 Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg  
 65 70 75 80  
 Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val  
 85 90 95

Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu  
 100 105 110  
 Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala  
 115 120 125  
 Pro Met Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu  
 130 135 140  
 Lys Ile Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu  
 145 150 155 160  
 Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr  
 165 170 175  
 Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser  
 180 185 190  
 Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro  
 195 200 205  
 Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu  
 210 215 220  
 Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val  
 225 230 235 240  
 Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp  
 245 250 255  
 Asp Ile Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly  
 260 265 270  
 Ile Leu Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser  
 275 280 285  
 Asp Thr His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn  
 290 295 300  
 Asp His Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr  
 305 310 315 320  
 Ser Asn Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu  
 325 330 335

&lt;210&gt; 78

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 78

Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser Tyr Asn Thr Ala  
 1 5 10 15  
 Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn Arg Ile Val Tyr  
 20 25 30  
 Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser Ala Cys Gly Val  
 35 40 45  
 Cys Pro Gly Lys Leu Arg Gly Val Arg Pro Val Arg Pro Lys Val Leu  
 50 55 60  
 Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg Ala Tyr Gly Gly  
 65 70 75 80  
 Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys Arg Ala Phe Leu  
 85 90 95  
 Ile Glu Glu Gln Lys Ile Ile Val Lys Val Leu Lys Ala Gln Ala Gln  
 100 105 110  
 Ser Gln Lys Ala Lys  
 115

&lt;210&gt; 79

&lt;211&gt; 614

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 79

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Arg Ser Gly Gln Pro Arg Ala Glu Gly Leu Gly Ala Gly Ala Ala Gly
 1           5           10           15
Pro Leu Arg Ala Met Ala Ala Pro Val Lys Gly Asn Arg Lys Gln Ser
      20           25           30
Thr Glu Gly Asp Ala Leu Asp Pro Pro Ala Ser Pro Lys Pro Ala Gly
      35           40           45
Lys Gln Asn Gly Ile Gln Asn Pro Ile Ser Leu Glu Asp Ser Pro Glu
      50           55           60
Ala Gly Gly Glu Arg Glu Glu Glu Gln Glu Arg Glu Glu Glu Gln Ala
65           70           75           80
Phe Leu Val Ser Leu Tyr Lys Phe Met Lys Glu Arg His Thr Pro Ile
      85           90           95
Glu Arg Val Pro His Leu Gly Phe Lys Gln Ile Asn Leu Trp Lys Ile
      100          105          110
Tyr Lys Ala Val Glu Lys Leu Gly Ala Tyr Glu Leu Val Thr Gly Arg
      115          120          125
Arg Leu Trp Lys Asn Val Tyr Asp Glu Leu Gly Gly Ser Pro Gly Ser
      130          135          140
Thr Ser Ala Ala Thr Cys Thr Arg Arg His Tyr Glu Arg Leu Val Leu
145          150          155          160
Pro Tyr Val Arg His Leu Lys Gly Glu Asp Asp Lys Pro Leu Pro Thr
      165          170          175
Ser Lys Pro Arg Lys Gln Tyr Lys Met Ala Lys Glu Asn Arg Gly Asp
      180          185          190
Asp Gly Ala Thr Glu Arg Pro Lys Lys Ala Lys Glu Glu Arg Arg Met
      195          200          205
Asp Gln Met Met Pro Gly Lys Thr Lys Ala Asp Ala Ala Asp Pro Ala
      210          215          220
Pro Leu Pro Ser Gln Glu Pro Pro Arg Asn Ser Thr Glu Gln Gln Gly
225          230          235          240
Leu Ala Ser Gly Ser Ser Val Ser Phe Val Gly Ala Ser Gly Cys Pro
      245          250          255
Glu Ala Tyr Lys Arg Leu Leu Ser Ser Phe Tyr Cys Lys Gly Thr His
      260          265          270
Gly Ile Met Ser Pro Leu Ala Lys Lys Lys Leu Leu Ala Gln Val Ser
      275          280          285
Lys Val Glu Ala Leu Gln Cys Gln Glu Glu Gly Cys Arg His Gly Ala
      290          295          300
Glu Pro Gln Ala Ser Pro Ala Val His Leu Pro Glu Ser Pro Gln Ser
305          310          315          320
Pro Lys Gly Leu Thr Glu Asn Ser Arg His Arg Leu Thr Pro Gln Glu
      325          330          335
Gly Leu Gln Ala Pro Gly Gly Ser Leu Arg Glu Glu Ala Gln Ala Gly
      340          345          350
Pro Cys Pro Ala Ala Pro Ile Phe Lys Gly Cys Phe Tyr Thr His Pro
      355          360          365
Thr Glu Val Leu Lys Pro Val Ser Gln His Pro Arg Asp Phe Phe Ser
      370          375          380
Arg Leu Lys Asp Gly Val Leu Leu Gly Pro : : Gly Lys Glu Gly Leu
385          390          400

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Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp Ala Asn Arg Pro  
 405 410 415  
 Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile Leu Tyr Pro Lys  
 420 425 430  
 Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val Pro Ala Glu Ser  
 435 440 445  
 Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly Leu Gly Ser Lys  
 450 455 460  
 Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly Lys Arg Leu Arg  
 465 470 475 480  
 Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys Lys Cys Gly Ala  
 485 490 495  
 Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu Gly Pro Ala Leu  
 500 505 510  
 Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met Leu His Cys Pro  
 515 520 525  
 Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly Gln Ala Ala Leu  
 530 535 540  
 Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala His Phe Leu Ala  
 545 550 555 560  
 Thr Ala Gly Pro Ser Pro Met Ala Ala Gly Leu Met His Phe Pro Pro  
 565 570 575  
 Thr Ser Phe Asp Ser Ala Leu Arg His Arg Leu Cys Pro Ala Ser Ser  
 580 585 590  
 Ala Trp His Ala Pro Pro Val Thr Thr Tyr Ala Ala Pro His Phe Phe  
 595 600 605  
 His Leu Asn Thr Lys Leu  
 610

<210> 80  
 <211> 114  
 <212> PRT  
 <213> Homo Sapiens

<400> 80  
 Met Ala Ser Val Ser Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu  
 1 5 10 15  
 His Asp Asp Glu Val Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile  
 20 25 30  
 Lys Ala Ala Gly Val Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala  
 35 40 45  
 Lys Ala Leu Ala Asn Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly  
 50 55 60  
 Ala Gly Gly Pro Ala Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro  
 65 70 75 80  
 Ala Pro Ser Thr Ala Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala  
 85 90 95  
 Lys Lys Glu Glu Ser Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu  
 100 105 110  
 Phe Asp

<210> 81  
 <211> 596  
 <212> PRT



&lt;213&gt; Homo Sapiens

&lt;400&gt; 81

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Met Arg Arg Ala His Glu Gly Arg Glu Ile Pro Ser Leu Gly Gly Ala
 1              5              10              15
Arg Arg Arg Glu Val Leu Gln Ala Gly Arg Ser Gln Arg Ala Ala Gly
      20              25              30
Arg Arg Arg Arg Arg Gln Glu Leu Glu Leu Gly Val Gly Ser Gly Arg
      35              40              45
Pro Gly Gly Pro Pro Pro Gly Pro Gly Arg Arg Gly Thr Cys Ala Ala
      50              55              60
Ala Leu Pro Pro Glu Trp Pro Arg Arg Arg Thr Gly Leu Pro Arg Arg
65              70              75              80
Gly Pro Arg Pro Pro Leu Ala Met Ala Lys Trp Leu Asn Lys Tyr Phe
      85              90              95
Ser Leu Gly Asn Ser Lys Thr Lys Ser Pro Pro Gln Pro Pro Arg Pro
      100              105              110
Asp Tyr Arg Glu Gln Arg Arg Arg Gly Glu Arg Pro Ser Gln Pro Pro
      115              120              125
Gln Ala Val Pro Gln Ala Ser Ser Ala Ala Ser Ala Ser Cys Gly Pro
      130              135              140
Ala Thr Ala Ser Cys Phe Ser Ala Ser Ser Gly Ser Leu Pro Asp Asp
145              150              155              160
Ser Gly Ser Thr Ser Asp Leu Ile Arg Ala Tyr Arg Ala Gln Lys Glu
      165              170              175
Arg His Phe Gln Asp Pro Tyr Asn Gly Pro Gly Ser Ser Leu Arg Lys
      180              185              190
Leu Arg Ala Met Cys Arg Leu Asp Tyr Cys Gly Gly Ser Gly Glu Pro
      195              200              205
Gly Gly Val Gln Arg Ala Phe Ser Ala Ser Ser Ala Ser Gly Ala Ala
      210              215              220
Gly Cys Cys Cys Ala Ser Ser Gly Ala Gly Ala Ala Ala Ser Ser Ser
225              230              235              240
Ser Ser Ser Gly Ser Pro His Leu Tyr Arg Ser Ser Ser Glu Arg Arg
      245              250              255
Pro Ala Thr Pro Ala Glu Val Arg Tyr Ile Ser Pro Lys His Arg Leu
      260              265              270
Ile Lys Val Glu Ser Ala Ala Gly Gly Gly Ala Gly Asp Pro Leu Gly
      275              280              285
Gly Ala Cys Ala Gly Gly Arg Thr Trp Ser Pro Thr Ala Cys Gly Gly
      290              295              300
Lys Lys Leu Leu Asn Lys Cys Ala Ala Ser Ala Ala Glu Glu Ser Gly
305              310              315              320
Ala Gly Lys Lys Asp Lys Val Thr Ile Ala Asp Asp Tyr Ser Asp Pro
      325              330              335
Phe Asp Ala Lys Asn Asp Leu Lys Ser Lys Ala Gly Lys Gly Glu Ser
      340              345              350
Ala Gly Tyr Met Glu Pro Tyr Glu Ala Gln Arg Ile Met Thr Glu Phe
      355              360              365
Gln Arg Gln Glu Ser Val Arg Ser Gln His Lys Gly Ile Gln Leu Tyr
      370              375              380
Asp Thr Pro Tyr Glu Pro Glu Gly Gln Ser Val Asp Ser Asp Ser Glu
385              390              395              400
Ser Thr Val Ser Pro Arg Leu Arg Glu Ser Lys Leu Pro Gln Asp Asp
      405              410              415

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Asp Arg Pro Ala Asp Glu Tyr Asp Gln Pro Trp Glu Trp Asn Arg Val  
 420 425 430  
 Thr Ser Pro Ala Leu Ala Ala Gln Phe Asn Gly Asn Glu Lys Arg Gln  
 435 440 445  
 Ser Ser Pro Ser Pro Ser Arg Asp Arg Arg Arg Gln Leu Arg Ala Pro  
 450 455 460  
 Gly Gly Gly Phe Lys Pro Ile Lys His Gly Ser Pro Glu Phe Cys Gly  
 465 470 475 480  
 Ile Leu Gly Glu Arg Val Asp Pro Ala Val Pro Leu Glu Lys Gln Ile  
 485 490 495  
 Trp Tyr His Gly Ala Ile Ser Arg Gly Asp Ala Glu Asn Leu Leu Arg  
 500 505 510  
 Leu Cys Lys Glu Cys Ser Tyr Leu Val Arg Asn Ser Gln Thr Ser Lys  
 515 520 525  
 His Asp Tyr Pro Leu Ser Leu Arg Ser Asn Gln Gly Phe Met His Met  
 530 535 540  
 Lys Leu Ala Lys Thr Lys Glu Lys Tyr Val Leu Gly Gln Asn Ser Pro  
 545 550 555 560  
 Pro Phe Asp Ser Val Pro Glu Val Ile His Tyr Tyr Thr Thr Arg Lys  
 565 570 575  
 Leu Pro Ile Lys Gly Ala Glu His Leu Ser Leu Leu Tyr Pro Val Ala  
 580 585 590  
 Val Arg Thr Leu  
 595

&lt;210&gt; 82

&lt;211&gt; 207

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 82

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
 1 5 10 15  
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
 20 25 30  
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 50 55 60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125  
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg  
 130 135 140  
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro  
 145 150 155 160  
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala  
 165 170 175  
 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala  
 180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala  
 195 200 205

<210> 83  
 <211> 429  
 <212> PRT  
 <213> Homo Sapiens

<400> 83

Glu Cys Asp Val Met Thr Tyr Val Arg Glu Thr Cys Gly Cys Cys Asp  
 1 5 10 15  
 Cys Glu Lys Arg Cys Gly Ala Leu Asp Val Val Phe Val Ile Asp Ser  
 20 25 30  
 Ser Glu Ser Ile Gly Tyr Thr Asn Phe Thr Leu Glu Lys Asn Phe Val  
 35 40 45  
 Ile Asn Val Val Asn Arg Leu Gly Ala Ile Ala Lys Asp Pro Lys Ser  
 50 55 60  
 Glu Thr Gly Thr Arg Val Gly Val Val Gln Tyr Ser His Glu Gly Thr  
 65 70 75 80  
 Phe Glu Ala Ile Gln Leu Asp Asp Glu His Ile Asp Ser Leu Ser Ser  
 85 90 95  
 Phe Lys Glu Ala Val Lys Asn Leu Glu Trp Ile Ala Gly Gly Thr Trp  
 100 105 110  
 Thr Pro Ser Ala Leu Lys Phe Ala Tyr Asp Arg Leu Ile Lys Glu Ser  
 115 120 125  
 Arg Arg Gln Lys Thr Arg Val Phe Ala Val Val Ile Thr Asp Gly Arg  
 130 135 140  
 His Asp Pro Arg Asp Asp Asp Leu Asn Leu Arg Ala Leu Cys Asp Arg  
 145 150 155 160  
 Asp Val Thr Val Thr Ala Ile Gly Ile Gly Asp Met Phe His Glu Lys  
 165 170 175  
 His Glu Ser Glu Asn Leu Tyr Ser Ile Ala Cys Asp Lys Pro Gln Gln  
 180 185 190  
 Val Arg Asn Met Thr Leu Phe Ser Asp Leu Val Ala Glu Lys Phe Ile  
 195 200 205  
 Asp Asp Met Glu Asp Val Leu Cys Pro Asp Pro Gln Ile Val Cys Pro  
 210 215 220  
 Asp Leu Pro Cys Gln Thr Glu Leu Ser Val Ala Gln Cys Thr Gln Arg  
 225 230 235 240  
 Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu Gly Glu  
 245 250 255  
 Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala Arg Arg  
 260 265 270  
 Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg Val Ala  
 275 280 285  
 Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe Pro Leu  
 290 295 300  
 Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr Gln Tyr  
 305 310 315 320  
 Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala Ile Asn  
 325 330 335  
 Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala Glu Leu  
 340 345 350  
 Ser Phe Val Phe Leu Thr Asp Gly Val Thr Gly Asn Asp Ser Leu His  
 355 360 365

Glu Ser Ala His Ser Met Arg Asn Glu Asn Val Val Pro Thr Val Leu  
 370 375 380  
 Ala Leu Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu  
 385 390 395 400  
 Gly Asp Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala  
 405 410 415  
 Gln Pro Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys  
 420 425

<210> 84  
 <211> 113  
 <212> PRT  
 <213> Homo Sapiens

<400> 84  
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr  
 1 5 10 15  
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu  
 20 25 30  
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val  
 35 40 45  
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val  
 50 55 60  
 Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln  
 65 70 75 80  
 Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp  
 85 90 95  
 Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Phe Val  
 100 105 110  
 Gly

<210> 85  
 <211> 258  
 <212> PRT  
 <213> Homo Sapiens

<400> 85  
 Met Ile Asn Ile Glu Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly  
 1 5 10 15  
 Arg Leu Glu Tyr Thr Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu  
 20 25 30  
 Ala His Ser Gln Ile Glu Lys Arg Arg Asp Lys Met Asn Ser Phe  
 35 40 45  
 Ile Asp Glu Leu Ala Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg  
 50 55 60  
 Lys Leu Asp Lys Leu Thr Val Leu Arg Met Ala Val Gln His Met Lys  
 65 70 75 80  
 Thr Leu Arg Gly Ala Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro  
 85 90 95  
 Thr Phe Leu Ser Asp Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala  
 100 105 110  
 Asp Gly Phe Leu Phe Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe  
 115 120 125  
 Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu

130		135		140
Ile Gly Gln Ser Leu Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys				
145		150		155
Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu				160
		165		170
Ile Asp Ala Lys Thr Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly				175
		180		185
Pro Ser Arg Leu Cys Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met				190
		195		200
Lys Cys Asn Arg Pro Ser Val Asn Val Glu Asp Lys Asn Phe Pro Ser				205
		210		215
Thr Cys Ser Lys Lys Lys Ala Asp Arg Lys Ala Phe Cys Thr Ile His				220
225		230		235
Ser Thr Gly Tyr Phe Gly Ile Phe Thr Thr Arg Thr Ser Arg His Ile				240
		245		250
				255
Val Leu				

&lt;210&gt; 86

&lt;211&gt; 569

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 86

Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr				
1		5		10
Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu				15
		20		25
Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr				30
		35		40
Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys				45
		50		55
Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser				60
65		70		75
Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu				80
		85		90
Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu				95
		100		105
Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln				110
		115		120
Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu				125
		130		135
Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser				140
145		150		155
Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe				160
		165		170
Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser				175
		180		185
Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg				190
		195		200
Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg				205
		210		215
Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu				220
225		230		235
Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile				240

245 250 255  
 Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn  
 260 265 270  
 Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp  
 275 280 285  
 His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly  
 290 295 300  
 Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu  
 305 310 315 320  
 Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys  
 325 330 335  
 Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu  
 340 345 350  
 Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys  
 355 360 365  
 Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala  
 370 375 380  
 Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr  
 385 390 395 400  
 Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp  
 405 410 415  
 Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys  
 420 425 430  
 Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp  
 435 440 445  
 Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys  
 450 455 460  
 Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu  
 465 470 475 480  
 Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn  
 485 490 495  
 Val His Lys Gln Arg Val Ala Glu Val Leu Asn Asp Pro Glu Asn Met  
 500 505 510  
 Glu Lys Arg Arg Ser Arg Glu Ser Leu Asn Val Asp Val Val Lys Tyr  
 515 520 525  
 Glu Ser Gly Pro Asp Gly Gly Glu Glu Val Ser Met Ser Val Glu Trp  
 530 535 540  
 Asn Gly Gly Val Ser Gly Arg Ala Ser Phe Cys Gly Lys Arg Gln Gln  
 545 550 555 560  
 Gln Gln Trp Pro Gly Arg Arg His Arg  
 565

&lt;210&gt; 87

&lt;211&gt; 736

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 87

Met Glu Ala Leu Ile Pro Val Ile Asn Lys Leu Gln Asp Val Phe Asn  
 1 5 10 15  
 Thr Val Gly Ala Asp Ile Ile Gln Leu Pro Gln Ile Val Val Val Gly  
 20 25 30  
 Thr Gln Ser Ser Gly Lys Ser Ser Val Leu Glu Ser Leu Val Gly Arg  
 35 40 45  
 Asp Leu Leu Pro Arg Gly Thr Gly Ile Val Thr Arg Arg Pro Leu Ile

50	55	60
Leu Gln Leu Val His Val Thr Gln Glu Asp Lys Arg Lys Thr Thr Gly		
65	70	75
Glu Glu Asn Gly Val Glu Ala Glu Glu Trp Gly Lys Phe Leu His Thr		80
	85	90
Lys Asn Lys Leu Tyr Thr Asp Phe Asp Glu Ile Arg Gln Glu Ile Glu		95
	100	105
Asn Glu Thr Glu Arg Ile Ser Gly Asn Asn Lys Gly Val Ser Pro Glu		110
	115	120
Pro Ile His Leu Lys Ile Phe Ser Pro Asn Val Val Asn Leu Thr Leu		125
	130	135
Val Asp Leu Pro Gly Met Thr Lys Val Pro Val Gly Asp Gln Pro Lys		140
145	150	155
Asp Ile Glu Leu Gln Ile Arg Glu Leu Ile Leu Arg Phe Ile Ser Asn		160
	165	170
Pro Asn Ser Ile Ile Leu Ala Val Thr Ala Ala Asn Thr Asp Met Ala		175
	180	185
Thr Ser Glu Ala Leu Lys Ile Ser Arg Glu Val Asp Pro Asp Gly Arg		190
	195	200
Arg Thr Leu Ala Val Ile Thr Lys Leu Asp Leu Met Asp Ala Gly Thr		205
	210	215
Asp Ala Met Asp Val Leu Met Gly Arg Val Ile Pro Val Lys Leu Gly		220
225	230	235
Ile Ile Gly Val Val Asn Arg Ser Gln Leu Asp Ile Asn Asn Lys Lys		240
	245	250
Ser Val Thr Asp Ser Ile Arg Asp Glu Tyr Ala Phe Leu Gln Lys Lys		255
	260	265
Tyr Pro Ser Leu Ala Asn Arg Asn Gly Thr Lys Tyr Leu Ala Arg Thr		270
	275	280
Leu Asn Arg Leu Leu Met His His Ile Arg Asp Cys Leu Pro Glu Leu		285
	290	295
Lys Thr Arg Ile Asn Val Leu Ala Ala Gln Tyr Gln Ser Leu Leu Asn		300
305	310	315
Ser Tyr Gly Glu Pro Val Asp Asp Lys Ser Ala Thr Leu Leu Gln Leu		320
	325	330
Ile Thr Lys Phe Ala Thr Glu Tyr Cys Asn Thr Ile Glu Gly Thr Ala		335
	340	345
Lys Tyr Ile Glu Thr Ser Glu Leu Cys Gly Gly Ala Arg Ile Cys Tyr		350
	355	360
Ile Phe His Glu Thr Phe Gly Arg Thr Leu Glu Ser Val Asp Pro Leu		365
	370	375
Gly Gly Leu Asn Thr Ile Asp Ile Leu Thr Ala Ile Arg Asn Ala Thr		380
385	390	395
Gly Pro Arg Pro Ala Leu Phe Val Pro Glu Val Ser Phe Glu Leu Leu		400
	405	410
Val Lys Arg Gln Ile Lys Arg Leu Glu Glu Pro Ser Leu Arg Cys Val		415
	420	425
Glu Leu Val His Glu Glu Met Gln Arg Ile Ile Gln His Cys Ser Asn		430
	435	440
Tyr Ser Thr Gln Glu Leu Leu Arg Phe Pro Lys Leu His Asp Ala Ile		445
	450	455
Val Glu Val Val Thr Cys Leu Leu Arg Lys Arg Leu Pro Val Thr Asn		460
465	470	475
Glu Met Val His Asn Leu Val Ala Ile Glu Leu Ala Tyr Ile Asn Thr		480
	485	490
		495

Lys His Pro Asp Phe Ala Asp Ala Cys Gly Leu Met Asn Asn Asn Ile  
 500 505 510  
 Glu Glu Gln Arg Arg Asn Arg Leu Ala Arg Glu Leu Pro Ser Ala Val  
 515 520 525  
 Ser Arg Asp Lys Ser Ser Lys Val Pro Ser Ala Leu Ala Pro Ala Ser  
 530 535 540  
 Gln Glu Pro Ser Pro Ala Ala Ser Ala Glu Ala Asp Gly Lys Leu Ile  
 545 550 555 560  
 Gln Asp Ser Arg Arg Glu Thr Lys Asn Val Ala Ser Gly Gly Gly Gly  
 565 570 575  
 Val Gly Asp Gly Val Gln Glu Pro Thr Thr Gly Asn Trp Arg Gly Met  
 580 585 590  
 Leu Lys Thr Ser Lys Ala Glu Glu Leu Leu Ala Glu Glu Lys Ser Lys  
 595 600 605  
 Pro Ile Pro Ile Met Pro Ala Ser Pro Gln Lys Gly His Ala Val Asn  
 610 615 620  
 Leu Leu Asp Val Pro Val Pro Val Ala Arg Lys Leu Ser Ala Arg Glu  
 625 630 635 640  
 Gln Arg Asp Cys Glu Val Ile Glu Arg Leu Ile Lys Ser Tyr Phe Leu  
 645 650 655  
 Ile Val Arg Lys Asn Ile Gln Asp Ser Val Pro Lys Ala Val Met His  
 660 665 670  
 Phe Leu Val Asn His Val Lys Asp Thr Leu Gln Ser Glu Leu Val Gly  
 675 680 685  
 Gln Leu Tyr Lys Ser Ser Leu Leu Asp Asp Leu Leu Thr Glu Ser Glu  
 690 695 700  
 Asp Met Ala Gln Arg Arg Lys Glu Ala Ala Asp Met Leu Lys Ala Leu  
 705 710 715 720  
 Gln Gly Ala Ser Gln Ile Ile Ala Glu Ile Arg Glu Thr His Leu Trp  
 725 730 735

<210> 88  
 <211> 37  
 <212> PRT  
 <213> Homo Sapiens

<400> 88  
 Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Phe Leu Ala Gly Gly  
 1 5 10 15  
 Val Ala Ala Ala Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val  
 20 25 30  
 Lys Leu Leu Leu Gln  
 35

<210> 89  
 <211> 1381  
 <212> DNA  
 <213> Homo Sapiens

<400> 89  
 ccgcagccct agagccgccc aagggatggc gatggcgctac ttggcttgga gactggcgcg 60  
 gcgttcgtgt ccgagttctc tgcaggtcnc tantttcccg gtagttcanc tgcncatgaa 120  
 tanaacagca atgagagccn ctcncaaaga ctttgaaaat tcaactgaatc nagtgaaact 180  
 ctngaaaaag gatccangaa acgaaatgaa nctnaaaat tgcagcgtat atnancangc 240  
 cncctgaanga cttgtntcat gccnaacca ngtgtntc tcttgatena caagggggcca 300



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atgggacaca tgggaatgcc ttggcancct gccnaagaa ctgccaggca naactatgtg      360
gatttggtgt ccantttgan tccntccttg gaatcctcna atcnngtgga ncctggaaca      420
nacaggaaat ccaactgggtt tgaaactctg gtggtgacct ccgaagatgg catcacaaag      480
atcatgttca accggcccaa aaagaaaaat gccataaaca ctgagatgta tcatgaaatt      540
atgctgtcac ttaaagctgc cagcaaggat gactcaatca tcaactgttt aacaggaaat      600
ggtgactatt acagtagtgg gaatgatctg actaacttca ctgatattcc ccctggtgga      660
gtagaggaga aagctaaaaa taatgccgtt ttactgaggg aatttggtgg ctgttttata      720
gattttccta agcctctgat tgcagtggtc aatggtccag ctgtgggcat ctcggtcacc      780
ctccttgggc tattcgatgc cgtgtatgca tctgacaggg caacatttca tacaccattt      840
agtcacctag gccaaagtcc ggaaggatgc tcctcttaca cttttccgaa gataatgagc      900
ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt      960
gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc     1020
aggctgaagg catttgcaaa gcttccccca aatgccttga gaatttcaaa agaggtaatc     1080
aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgtccttcag     1140
ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttata cagaaaatca     1200
aaactgtgat gaccactaca gcagagtaaa gcatgtccaa ggaaggatgt gctgttacct     1260
ctgatttcca gtactggaac taaataagct tcattgtgcc ttttgtagtg ctagaatatc     1320
aattacaatg atgatatttc actacagctc tgatgaataa aaagttttgt aaaacaagaa     1380
a                                                                                   1381

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&lt;210&gt; 90

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 90

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Thr Cys Met Pro Pro Val Phe Asp Leu Ile Lys Gly Pro Met Gly His
 1           5           10          15
Met Glu Cys Pro Trp Pro Ala Arg Thr Ala Arg Asn Tyr Val Asp Leu
          20          25          30
Val Ser Leu Pro Ser Leu Glu Ser Ser Asn Val Pro Gly Thr Arg Lys
          35          40          45
Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr
          50          55          60
Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu
65          70          75          80
Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
          85          90          95
Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
          100         105         110
Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
          115         120         125
Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
          130         135         140
Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
145         150         155         160
Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
          165         170         175
Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
          180         185         190
Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
          195         200         205
Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
210         215         220
Cys Ala Gln Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys

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<210> 91
<211> 1514
<212> DNA
<213> Homo Sapiens
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<210> 92
<211> 407
<212> PRT
<213> Homo Sapiens
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Thr Ala Met Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile  
 50 55 60  
 Gly Phe Ser Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp  
 65 70 75 80  
 Thr Ala Met Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu  
 85 90 95  
 Pro His Phe Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly  
 100 105 110  
 Ser Thr Pro Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly  
 115 120 125  
 Ile Asp Phe Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr  
 130 135 140  
 Gln Ser Ser Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu  
 145 150 155 160  
 Gly Gly Ala Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu  
 165 170 175  
 Asn Lys Ala Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu  
 180 185 190  
 Lys Leu Gly Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly  
 195 200 205  
 Ser Ala Val Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn  
 210 215 220  
 Ser Leu Pro Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala  
 225 230 235 240  
 Asp Ile Ala Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys  
 245 250 255  
 Asn Gly Ile Ala Gly Ser Ser Leu Pro Pro Pro Pro Ile Lys His Asn  
 260 265 270  
 Met Asp Ile Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro  
 275 280 285  
 Ser Gln Ala Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro  
 290 295 300  
 Gln Pro Val Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala  
 305 310 315 320  
 Ser Val Gly Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Gln Pro  
 325 330 335  
 Ala Gln Leu Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val  
 340 345 350  
 Ala Pro Arg Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly  
 355 360 365  
 Asn Gly Val Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu  
 370 375 380  
 Pro His Pro Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro  
 385 390 395 400  
 Lys Asp Phe Asp Trp Glu Ile  
 405

&lt;210&gt; 93

&lt;211&gt; 2236

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 93

cctggcccggtcgcgggtcgc ggcctctttcc agctcctggg agccggggcac ccgaaggaac 60  
 gggtcgtgca acgacgcagc tggacctggc ccagcctggg agcgaaaagt ggcccgagaa 120

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ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tctgaggaga cctgaagctg 240
gtcatcaatg aaccacagccg tctgcctctg tttgatgcca ttcggccgct gatccactg 300
aagcaccagg tggaatatga tcagctgacc ccccggcgct ccaggaagct gaaggaggtg 360
cgtctggacc gtctgcaccc cgaaggcctc ggcctgagtg tgcgtggtgg cctggagttt 420
ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg taccatgag 540
gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagttag acacatcggc 600
ctgatccccg tgaaaagctc tcctgatgag cccctcactt ggcagtatgt ggatcagttt 660
gtgtcggaat ctgggggctg gcgaggcagc ctgggctccc ctggaaatcg ggaaaacaag 720
gagaagaagg tcttcatcag cctggtaggc tcccgaggcc ttggctgcag catttccagc 780
ggccccatcc agaagcctgg catctttatc agccatgtga aacctggctc cctgtctgct 840
gaggtgggat tggagatagg ggaccagatt gtcgaagtca atggcgtcga cttctctaac 900
ctggatcaca aggaggtgt aaatgtgctg aaaaatagcc gcagcctgac catctccatt 960
gtagctgcag ctggccggga gctgttcatg acagaccggg agcggctggc agaggcgagg 1020
cagcgtgagc tgcagcgga ggagcttctc atgcagaagc ggctggcgat ggagtccaac 1080
aagatcctcc aggagcagca ggagatggag cggcaaagga gaaaagaaat tgcccagaag 1140
gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggaagag 1200
aagtttaaga agcaatggga agaagactgg ggctcaaagg aacagctact cttgcctaaa 1260
accatcactg ctgaggtaca cccagtaccc cttcgcaagc caaagtatga tcagggagtg 1320
gaacctgagc tcgagcccg acatgacctg gatggaggca cggaggagca gggagagcag 1380
gatttccgga aatatgagga aggctttgac ccctactcta tggtcacccc agagcagatc 1440
atggggaagg atgtccggct cctacgcac aagaaggagg gatccttaga cctggccctg 1500
gaaggcggtg tggactcccc cattgggaag gtggtcgttt ctgctgtgta tgagcgggga 1560
gctgctgagc ggcattggtg cattgtgaaa ggggacgaga tcatggcaat caacggcaag 1620
attgtgacag actacacct ggctgaggct gacgctgccc tgcagaaggc ctggaatcag 1680
ggcgggggact ggatcgacct tgtggttgcc gtctgcccc caaaggagta tgacgatgag 1740
ctgaccttct tgctgaagtc caaaagggga aaccaaattc acgcgttagg aaacagttag 1800
ctccggcccc acctcgtgaa cacaaagcct cggaccagcc ttgagagagg ccacatgaca 1860
cacaccagat ggcacacctg ggacctgaat ctatcaccca ggaatctcaa actccctttg 1920
gccctgaacc agggccagat aaggaacagc tcgggcccact tttttgaagg ccaatgtgga 1980
ggaaagggag cagccagccg tttgggagaa gatctcaagg atccagactc tcattccttt 2040
cctctggccc agtgaatttg gtctctccca gctttggggg actccttctt tgaaccctaa 2100
taagacccca ctggagtctc tctctctcca tccctctcct ctgcccctctg ctctaattgc 2160
tgccaggatt gtcactccaa accttactct gagctcatta ataaaataaa cagattttatt 2220
ttccagctta aaaaaa 2236

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&lt;210&gt; 94

&lt;211&gt; 652

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 94

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Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
1          5          10          15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85          90          95

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Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu  
 100 105 110  
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu  
 115 120 125  
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser  
 130 135 140  
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val  
 145 150 155 160  
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro  
 165 170 175  
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser  
 180 185 190  
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys  
 195 200 205  
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys  
 210 215 220  
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His  
 225 230 235 240  
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp  
 245 250 255  
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys  
 260 265 270  
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile  
 275 280 285  
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu  
 290 295 300  
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln  
 305 310 315 320  
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu  
 325 330 335  
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu  
 340 345 350  
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu  
 355 360 365  
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu  
 370 375 380  
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg  
 385 390 395 400  
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp  
 405 410 415  
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys  
 420 425 430  
 Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile  
 435 440 445  
 Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu  
 450 455 460  
 Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val  
 465 470 475 480  
 Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile  
 485 490 495  
 Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp  
 500 505 510  
 Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln  
 515 520 525  
 Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu

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<210> 95
<211> 831
<212> DNA
<213> Homo Sapiens
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-> <210> 96
    <211> 184
    <212> PRT
    <213> Homo Sapiens

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-66-

Glu Asn Asn His Gly Phe His Glu Lys Thr Ala Ala Leu Lys Leu Glu  
 100 105 110  
 Ala Glu Gly Glu Ala Met Glu Asp Ala Ala Ala Pro Gly Asn Asp Arg  
 115 120 125  
 Gly Gly Thr Gln Glu Pro Ala Pro Val Pro Ala Glu Pro Phe Asp Asn  
 130 135 140  
 Thr Thr Tyr Lys Asn Leu Gln His His Asp Tyr Ser Thr Tyr Thr Phe  
 145 150 155 160  
 Leu Asp Leu Asn Leu Glu Leu Ser Lys Phe Arg Met Pro Gln Pro Ser  
 165 170 175  
 Ser Gly Arg Glu Ser Pro Arg His  
 180

<210> 97  
 <211> 1008  
 <212> DNA  
 <213> Homo Sapiens

<400> 97  
 gcaaggtctc caagtcaccag ctcaaggtcc tttcccataa cctgtgcacg gtgctgaagg 60  
 ttcctcatga cccagttgccc cttgaagagc acttcaggga tgatgatgag ggtccagtgt 120  
 ccaaccaggg ctacatgcct tatttaaaca ggttcatttt ggaaaagggtc caagacaact 180  
 ttgacaagat tgaattcaat aggatgtgtt ggaccctctg tgcataaaaaa aacctcacia 240  
 agaatccctt gctcattaca gaagaanatg catttaaaat atgggttatt ttcaactttt 300  
 tatctgagga caagtatcca ttaattattg tgtcagaana gattgaatac ctgcttaaga 360  
 agcttacaga agctatggga ggaggttggc agcaagaaca atttgaacat tataaaatca 420  
 actttgatga cagtaaaaaat ggcttttctg catgggaact tattgagctt attggaaatg 480  
 gacagtttag caaaggcatg gaccggcaga ctgtgtctat ggcaattaat gaagtcttta 540  
 atgaacttat attagatgtg ttaaagcagg gttacatgat gaaaaagggtc cacagacgga 600  
 aaaactggac tgaacgatgg tttgtactaa aacccaacat aatttcttac tatgtgagtg 660  
 aggatctgaa ggataagaaa ggagacattc tcttgatga aaattgctgt gtagagtcct 720  
 tgcttgacaa agatggaaaag aaatgccttt ttctcgtaaa atgttttgat aagacttttg 780  
 aaatcagtg cttcagataag aanaanaaac aggagtggat tcaagccatt cattctacta 840  
 ttcattctgtt gaagctgngc agccctccac canacaaaga agccnccag cttctnaaan 900  
 aactccggna gaatcatctg gctgaacaag angaactgga gcgacaaatg aangaactcc 960  
 aagcccgcga atgaaagcaa ncagcaagag ctggaaggcc ttncggaa 1008

<210> 98  
 <211> 312  
 <212> PRT  
 <213> Homo Sapiens

<400> 98  
 Lys Val Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Cys Thr  
 1 5 10 15  
 Val Leu Lys Val Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg  
 20 25 30  
 Asp Asp Asp Glu Gly Pro Val Ser Asn Gln Gly Tyr Met Pro Tyr Leu  
 35 40 45  
 Asn Arg Phe Ile Leu Glu Lys Val Gln Asp Asn Phe Asp Lys Ile Glu  
 50 55 60  
 Phe Asn Arg Met Cys Trp Thr Leu Cys Val Lys Lys Asn Leu Thr Lys  
 65 70 75 80  
 Asn Pro Leu Leu Ile Thr Glu Glu Ala Phe Lys Ile Trp Val Ile Phe  
 85 90 95

Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Ile Val Ser Glu Ile  
 100 105 110  
 Glu Tyr Leu Leu Lys Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln  
 115 120 125  
 Gln Glu Gln Phe Glu His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn  
 130 135 140  
 Gly Leu Ser Ala Trp Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe  
 145 150 155 160  
 Ser Lys Gly Met Asp Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val  
 165 170 175  
 Phe Asn Glu Leu Ile Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys  
 180 185 190  
 Lys Gly His Arg Arg Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys  
 195 200 205  
 Pro Asn Ile Ile Ser Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys  
 210 215 220  
 Gly Asp Ile Leu Leu Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp  
 225 230 235 240  
 Lys Asp Gly Lys Lys Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr  
 245 250 255  
 Phe Glu Ile Ser Ala Ser Asp Lys Lys Gln Glu Trp Ile Gln Ala Ile  
 260 265 270  
 His Ser Thr Ile His Leu Leu Lys Leu Ser Pro Pro Pro Lys Glu Ala  
 275 280 285  
 Gln Leu Leu Lys Leu Arg Asn His Leu Ala Glu Gln Glu Leu Glu Arg  
 290 295 300  
 Gln Met Glu Leu Gln Ala Arg Gln  
 305 310

<210> 99  
 <211> 1009  
 <212> DNA  
 <213> Homo Sapiens

<400> 99  
 ggctaagtga acatactcta ccacttggtc tgaagcccag cagtatctga tggataatcc 60  
 aacttttgca gaagatgagg agttacaaaa tatggacaaa gaagatgcat taatttgctt 120  
 tgaagaacac attcgggctt tagaaaaagga ggaagaagaa gaaaaacaga agagtttgct 180  
 gagagaaagg agacgacagc gaaaaaatag ggaatctttc cagatatttt tagatgaatt 240  
 acatgaacat ggacaactgc attctatgtc atcttggatg gaattgtatc caactattag 300  
 ttctgatatt agattcacta atatgcttgg tcagcctgga tcaactgcac ttgatctttt 360  
 caagttttat gttgaggatc ttaaagcacg ttatcatgac gagaagaaga taataaaaga 420  
 cattctaaag gataaaggat ttgtagtga agtaaacact acttttgaag attttgtggc 480  
 gataatcagt tcaactaaaa gatcaactac attagatgct ggaaatatca aattggcttt 540  
 caatagttta ctagaaaagg cagaagcccg tgaacgtgaa agagaaaaag aagaggctcg 600  
 gaagatgaaa cgaaaagaat ctgcatttaa gagtatgtta aaacaagctg ctctccgat 660  
 agaattggat gctgtctggg aagatatccg tgagagattt gtaaaagagc cagcatttga 720  
 ggacataact ctagaatctg aaagaaaacg aatattttaa gattttatgc atgtgcttga 780  
 gcatgaatgt cagcatcatc attcaaagaa caagaaacat tctaagaaat ctaaaaaaca 840  
 tcataggaaa cgttcccgcg ctcgatcggg gtcagattca ngatgatgat gatagccatt 900  
 caaagaaaaa aagacagcga tgagaagtct cgggtctgntt canaacattc ttccantngc 960  
 agagtctgag agaagtntaa aaagtcaaaa nagcatagan aggaaagtt 1009

<210> 100  
 <211> 292



&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 100

Ala Asn Val Thr Tyr Ser Thr Thr Trp Ser Glu Ala Gln Gln Tyr Leu  
 1 5 10 15  
 Met Asp Asn Pro Thr Phe Ala Glu Asp Glu Glu Leu Gln Asn Met Asp  
 20 25 30  
 Lys Glu Asp Ala Leu Ile Cys Phe Glu Glu His Ile Arg Ala Leu Glu  
 35 40 45  
 Lys Glu Glu Glu Glu Glu Lys Gln Lys Ser Leu Leu Arg Glu Arg Arg  
 50 55 60  
 Arg Gln Arg Lys Asn Arg Glu Ser Phe Gln Ile Phe Leu Asp Glu Leu  
 65 70 75 80  
 His Glu His Gly Gln Leu His Ser Met Ser Ser Trp Met Glu Leu Tyr  
 85 90 95  
 Pro Thr Ile Ser Ser Asp Ile Arg Phe Thr Asn Met Leu Gly Gln Pro  
 100 105 110  
 Gly Ser Thr Ala Leu Asp Leu Phe Lys Phe Tyr Val Glu Asp Leu Lys  
 115 120 125  
 Ala Arg Tyr His Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp  
 130 135 140  
 Lys Gly Phe Val Val Glu Val Asn Thr Thr Phe Glu Asp Phe Val Ala  
 145 150 155 160  
 Ile Ile Ser Ser Thr Lys Arg Ser Thr Thr Leu Asp Ala Gly Asn Ile  
 165 170 175  
 Lys Leu Ala Phe Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg  
 180 185 190  
 Glu Arg Glu Lys Glu Glu Ala Arg Lys Met Lys Arg Lys Glu Ser Ala  
 195 200 205  
 Phe Lys Ser Met Leu Lys Gln Ala Ala Pro Pro Ile Glu Leu Asp Ala  
 210 215 220  
 Val Trp Glu Asp Ile Arg Glu Arg Phe Val Lys Glu Pro Ala Phe Glu  
 225 230 235 240  
 Asp Ile Thr Leu Glu Ser Glu Arg Lys Arg Ile Phe Lys Asp Phe Met  
 245 250 255  
 His Val Leu Glu His Glu Cys Gln His His His Ser Lys Asn Lys Lys  
 260 265 270  
 His Ser Lys Lys Ser Lys Lys His His Arg Lys Arg Ser Arg Ser Arg  
 275 280 285  
 Ser Gly Ser Asp  
 290

&lt;210&gt; 101

&lt;211&gt; 983

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 101

agggtgacaat agatatagaa gtacgttgat gtgcgaagat gtattttggtt ttagccagcg 60  
 aggaaaaaag aatcagtttg attatacatt taccaaacat taagaattta atatggtaac 120  
 ttttattttca gtattaaaat agcaatttta ttattactt ttttatatat agaatttgac 180  
 accaaattttt ggaacttaaa aagaagattc ttaaaactta caatccagat tacgatgagg 240  
 acctggtgca ggaagcttca tctgaagatg tcctgggcgt tcatatggtg gacaaagaca 300  
 cagagagaga cattgagatg aaacggcaac tacggcgact acgggagctc cacctataca 360

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gcacatggaa gaagtaccaa gaggcgatga agacatcctt gggagttcca caacgtgagc 420
gtgacgaagg ctccttgggc aagccattgt gtccaccgga gatactctcg gagacgttgc 480
caggetctgt gaagaaaagg gtatgctttc catcagaaga tcatctagag gagtttatag 540
cagaacatct ccctgaagca tccaatcaga gtctcctcac tgttgcccat gcagacgcag 600
gcacccaaac caacggtgac ctggaagacc tggaggagca tgggccaggg cagacagtct 660
ctgaggaagc cacagaagtt cacatgatgg agggggaccc agacacactg gccgaacttc 720
tgatcagggg tgtacttcag gagctgtcca gttacaacgg cgaggaggag gacccanagg 780
aggtgaagac atccttggga gttccacaac gtggtgacct ggaagacctg gaggagcatg 840
tgncagggca gnnnttctct gaggaagcca caggggttca catgatgcag gtggaccag 900
ccacgctggc aaagagtgc ctggaagacc tggaggagca tgtgccagag cagacagtct 960
ctgaggaagc cacaggggtt cac 983

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&lt;210&gt; 102

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 102

```

Met Val Asp Lys Asp Thr Glu Arg Asp Ile Glu Met Lys Arg Gln Leu
 1             5             10             15
Arg Arg Leu Arg Glu Leu His Leu Tyr Ser Thr Trp Lys Lys Tyr Gln
      20             25             30
Glu Ala Met Lys Thr Ser Leu Gly Val Pro Gln Arg Glu Arg Asp Glu
      35             40             45
Gly Ser Leu Gly Lys Pro Leu Cys Pro Pro Glu Ile Leu Ser Glu Thr
      50             55             60
Leu Pro Gly Ser Val Lys Lys Arg Val Cys Phe Pro Ser Glu Asp His
      65             70             75             80
Leu Glu Glu Phe Ile Ala Glu His Leu Pro Glu Ala Ser Asn Gln Ser
      85             90             95
Leu Leu Thr Val Ala His Ala Asp Ala Gly Thr Gln Thr Asn Gly Asp
      100            105            110
Leu Glu Asp Leu Glu Glu His Gly Pro Gly Gln Thr Val Ser Glu Glu
      115            120            125
Ala Thr Glu Val His Met Met Glu Gly Asp Pro Asp Thr Leu Ala Glu
      130            135            140
Leu Leu Ile Arg Asp Val Leu Gln Glu Leu Ser Ser Tyr Asn Gly Glu
      145            150            155            160
Glu Glu Asp Pro Glu Val Lys Thr Ser Leu Gly Val Pro Gln Arg Gly
      165            170            175
Asp Leu Glu Asp Leu Glu Glu His Val Gly Gln Phe Ser Glu Glu Ala
      180            185            190
Thr Gly Val His Met Met Gln Val Asp Pro Ala Thr Leu Ala Lys Ser
      195            200            205
Asp Leu Glu Asp Leu Glu Glu His Val Pro Glu Gln Thr Val Ser Glu
      210            215            220
Glu Ala Thr Gly Val His
      225            230

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&lt;210&gt; 103

&lt;211&gt; 843

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 103

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aatncccgcct gcaggtcgac actagtggat ccaaagaatt cggcacgagg caagttctgg      60
gagctggaca cggaccacga cctgctcatc gacgcggacg acctggcgcg gcacaatgac      120
cacgcccttt ctaccaagat gatagacagg atcttctcag gagcagtcac acgaggcaga      180
aaagtgcaga aggaaggga gatcagctat gccgactttg tctggttttt gatctctgag      240
gaagacaaaa aaacaccgac cagcatcgag tacttggttc gctgcatgga cctggacggg      300
gacggcgccc tgtccatggt cgagctcgag tacttctacg aggagcagtg ccgaaggctg      360
gacagcatgg ccatcgaggc cctgcccttc caggactgcc tctgccagat gctggacctg      420
gtcaagccga ggactgaagg gaagatcacg ctgcaggacc tgaagcgctg caagctggcc      480
aacgtcttct tcgacacctt cttcaacatc gagaagtncc tcgaccacga gcagaaagag      540
cagatctccc tgctcagggg cggtagacagc ggcgggcccg agctctcgga ctgggagaag      600
tnccggccga agagtncgac atcctgggtg cggangaaac cgtggggana nccctgggga      660
agacgggttc naaggcgaac tcaccccnt ggancanaaa ctgantgcgc tgcgtcccc      720
gctggggccan aggccttctt ccaagcgct cccgctgggg cgcgctggaa ctgttncaaa      780
tccccctgcg gggacaagaa cttgaaaccg ctgtganncc ccccnana accnccccg      840
gnt                                                                    843

```

<210> 104  
 <211> 197  
 <212> PRT  
 <213> Homo Sapiens

```

<400> 104
Arg Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser Ala Arg Gly Lys
 1              5              10              15
Phe Trp Glu Leu Asp Thr Asp His Asp Leu Leu Ile Asp Ala Asp Asp
              20              25              30
Leu Ala Arg His Asn Asp His Ala Leu Ser Thr Lys Met Ile Asp Arg
              35              40              45
Ile Phe Ser Gly Ala Val Thr Arg Gly Arg Lys Val Gln Lys Glu Gly
              50              55              60
Lys Ile Ser Tyr Ala Asp Phe Val Trp Phe Leu Ile Ser Glu Glu Asp
              65              70              75              80
Lys Lys Thr Pro Thr Ser Ile Glu Tyr Trp Phe Arg Cys Met Asp Leu
              85              90              95
Asp Gly Asp Gly Ala Leu Ser Met Phe Glu Leu Glu Tyr Phe Tyr Glu
              100             105             110
Glu Gln Cys Arg Arg Leu Asp Ser Met Ala Ile Glu Ala Leu Pro Phe
              115             120             125
Gln Asp Cys Leu Cys Gln Met Leu Asp Leu Val Lys Pro Arg Thr Glu
              130             135             140
Gly Lys Ile Thr Leu Gln Asp Leu Lys Arg Cys Lys Leu Ala Asn Val
              145             150             155             160
Phe Phe Asp Thr Phe Phe Asn Ile Glu Lys Leu Asp His Glu Gln Lys
              165             170             175
Glu Gln Ile Ser Leu Leu Arg Asp Gly Asp Ser Gly Gly Pro Glu Leu
              180             185             190
Ser Asp Trp Glu Lys
              195

```

<210> 105  
 <211> 2264  
 <212> DNA  
 <213> Homo Sapiens

<400> 105

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atgcagtacc tgacacgtcc acttaccagt atgatgaatc ttcaggatat tactatgatc      120
cgacaacagg gctctattat gaccccaact cgcaatacta ctataattcc ttgaccagc      180
agtaccttta ctgggatggg gaaaaagaga cctacgtgcc agctgcagag tctagctccc      240
accagcagtc gggcctgctt cctgcaaaaag aggggaaaga gaagaaggag aaacccaaga      300
gcaaaacagc ccagcagatt gccaaagaca tggaaacgctg ggctaagagt ttgaataagc      360
agaaaagaaa ctttaaaaat agctttcagc ctgtcaattc cttgagggaa gaagaaagga      420
gagaatctgc tgcagcagac gctggctttg ctctctttga gaagaaggga gccttagctg      480
aaaggcagca gctcatccca gaattgggtg gaaatggaga tgaggagaat cccctcaaaa      540
ggggctctgg tgcctgttac agtgggtgaca gtgacaatga ggaggagctg gtggagagac      600
ttgagagtga ggaagagaag ctagtctgact ggaagaagat ggctgtctct ctctgccggc      660
gccagttccc gaacaaagat gccctagtca ggcaccagca actctcagac cttcacaagc      720
aaaacatgga catctaccga cgatccaggc tgagcgagca ggagctggaa gccttggagc      780
taaggagagag agagatgaaa taccgagacc gagctgcaga aagacgggag aagtacggca      840
ttccagaacc tccagagccc aagcgcaaga agcagtttga tgccggcact gtgaattacg      900
agcaaccacac caaagatggc attgaccaca gtaacattgg caacaagatg ctgcaggcca      960
tgggctggcg ggaaggctct ggcttgggac gaaagtgtca aggcattacg gctcccattg      1020
aggctcaagt tgggctaaaag ggagctggcc taggagccaa aggcagcgca tatggtttgt      1080
cgggcgcccga ttccatacaa gatgctgtcc ggaaagccat gtttgcccgg ttcactgaga      1140
tggagtgaga gagagagaga gagagagatg acaaggagca caagaagtgg tccatctccc      1200
gaattcgctg ttaccgcctg tctctttaag ggcattgcct gtgctgttaa tagatcttag      1260
gggtgaaccac ttcattctgc agggttctcc ctcccacctt aaagaagttc ccttatgtg      1320
ggttgcctgg tgaatggcct tccttcccgc cagagggctt gtgaacagac cggagaggac      1380
agtggattgt ttatactcca gtgtacatag tgtaatgtag cgtgtttaca tgtgtagcct      1440
atgttgtggt ccacacagccc ctcacattcc taggggtttg agatgctgta ggtggtatgt      1500
gacaccaaag ccacctctgt catttgttgt gatgtctttt cttggcaaaa gccttgtgta      1560
tatttgtata ttacacattt gtacagaatt ttggaagatt ttcaatccaa gttgccaaat      1620
ctggctcctt tacaaaagaa ataccttgag aaaaaaaann aannaaaaaa aannccnann      1680
nnntttttaa aanggnncgg gggccaannn ttttccnncc gggnggggna nnaagtaaan      1740
ngtcccaaat nccccaaaaa nggagccenn ttaaaattaa angggccgcn nttttaaaaa      1800
nttcngaantn gggnaaaacc tnggggtttt ccaaatttaa cccctttgaa aaaaaanccc      1860
ctttcncaaa anngggnntaa tanccaaaaa gggcccccann ccatttttgc ccnttccaaa      1920
aaaatttgnc caanncnnaa atgggnnaaan ggggaatcca attttttaaa gggnnaaaaa      1980
gggttttaaac nnacgggnnt ccaaanttgn ttgggggaat ttttaaattc ccaannnccc      2040
aaggggggnc atttagnngn cccnaaatcc cccaaaaant ggttcnnggn tnaaanengc      2100
cnnnnccnaa tttntanggg tttacttngn tttaaaaaac cccccaaaaa actccccenn      2160
gaaccnaaaa aanaaaagga ngccattttt ngngnnaaac ttttttaann nncennntaa      2220
anggggttaa aaannnnnnn tnnncccnnaa tttttcaaan aang      2264

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&lt;210&gt; 106

&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 106

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Ser Thr Ser Thr Gln Ala Pro Ala Ala Ser Pro Thr Gly Val Val Pro
 1          5          10          15
Gly Thr Lys Tyr Ala Val Pro Asp Thr Ser Thr Tyr Gln Tyr Asp Glu
          20          25          30
Ser Ser Gly Tyr Tyr Tyr Asp Pro Thr Thr Gly Leu Tyr Tyr Asp Pro
          35          40          45
Asn Ser Gln Tyr Tyr Tyr Asn Ser Leu Thr Gln Gln Tyr Leu Tyr Trp
          50          55          60
Asp Gly Glu Lys Glu Thr Tyr Val Pro Ala Ala Glu Ser Ser Ser His
65          70          80

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Gln Gln Ser Gly Leu Pro Pro Ala Lys Glu Gly Lys Glu Lys Lys Glu  
 85 90 95  
 Lys Pro Lys Ser Lys Thr Ala Gln Gln Ile Ala Lys Asp Met Glu Arg  
 100 105 110  
 Trp Ala Lys Ser Leu Asn Lys Gln Lys Glu Asn Phe Lys Asn Ser Phe  
 115 120 125  
 Gln Pro Val Asn Ser Leu Arg Glu Glu Glu Arg Arg Glu Ser Ala Ala  
 130 135 140  
 Ala Asp Ala Gly Phe Ala Leu Phe Glu Lys Lys Gly Ala Leu Ala Glu  
 145 150 155 160  
 Arg Gln Gln Leu Ile Pro Glu Leu Val Arg Asn Gly Asp Glu Glu Asn  
 165 170 175  
 Pro Leu Lys Arg Gly Leu Val Ala Ala Tyr Ser Gly Asp Ser Asp Asn  
 180 185 190  
 Glu Glu Glu Leu Val Glu Arg Leu Glu Ser Glu Glu Glu Lys Leu Ala  
 195 200 205  
 Asp Trp Lys Lys Met Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro Asn  
 210 215 220  
 Lys Asp Ala Leu Val Arg His Gln Gln Leu Ser Asp Leu His Lys Gln  
 225 230 235 240  
 Asn Met Asp Ile Tyr Arg Arg Ser Arg Leu Ser Glu Gln Glu Leu Glu  
 245 250 255  
 Ala Leu Glu Leu Arg Glu Arg Glu Met Lys Tyr Arg Asp Arg Ala Ala  
 260 265 270  
 Glu Arg Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg  
 275 280 285  
 Lys Lys Gln Phe Asp Ala Gly Thr Val Asn Tyr Glu Gln Pro Thr Lys  
 290 295 300  
 Asp Gly Ile Asp His Ser Asn Ile Gly Asn Lys Met Leu Gln Ala Met  
 305 310 315 320  
 Gly Trp Arg Glu Gly Ser Gly Leu Gly Arg Lys Cys Gln Gly Ile Thr  
 325 330 335  
 Ala Pro Ile Glu Ala Gln Val Arg Leu Lys Gly Ala Gly Leu Gly Ala  
 340 345 350  
 Lys Gly Ser Ala Tyr Gly Leu Ser Gly Ala Asp Ser Tyr Lys Asp Ala  
 355 360 365  
 Val Arg Lys Ala Met Phe Ala Arg Phe Thr Glu Met Glu  
 370 375 380

&lt;210&gt; 107

&lt;211&gt; 1367

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 107

gcgacacagg	cctcgaggct	gtctctgaca	agtgttcaca	ggaggtgggg	acgcctctgc	60
gcgaggaacg	aggagctacg	ggcctgggcc	cggttattgc	catgggcagc	ggctgccgca	120
tcgaatgcat	attcttcagc	gagttccacc	ccacgctggg	acccaagatc	acctatcagg	180
tccctgaaga	cttcatctcc	cgagagctgt	ttgacacagt	ccaagtgtac	atcatcacca	240
agccagagct	gcagaacaag	cttatcactg	tcacagctat	ggaaaagaag	ctgatcggtc	300
gtcctgtgtg	catcgaaacac	aagaagtaca	gccgcaatgc	tctcctcttc	aacctgggct	360
tcgtgtgtga	tgcccaggcc	aagacctgcg	ccctcgagcc	cattgttaaa	aagctggctg	420
gctatctgac	cacactagag	ctagagagca	gcttcgtggt	catggaggag	agcaagcaga	480
agttgggtgcc	catcatgacc	atcttgctgg	aggagctaac	tgcttcaggc	cggtgcactc	540
tgcccattga	tgagtccaac	accatccact	tgaagctaac	ggagcagcgg	ccagaccctc	600

```

cggtggccca ggagtatgat gtacctgtct ttaccaaaga caaggaggat ttcttcaact 660
cacagtggga cctcactaca caacaaatcc tgcctacat tgatgggttc cgccacatcc 720
agaagatttc agcagaggca gatgtggagc tcaacctggt gcgcattget atccagaacc 780
tgctgtacta cggcgttgtg acactggtgt ccactcctcca gtactccaat gtatactgcc 840
caacgccc aa ggtccaggac ctggtagatg acaagtccct gcaagaggca tgtctatcct 900
acgtgaccaa gcaagggcac aagagggcca gtctccggga tgtgttccag ctatactgca 960
gcctgagccc tggcactacc gtgcgagacc tcattggccg ccacccccag cagctgcagc 1020
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agcggcttga aaatgacccc aacatcatca tctgctggaa gtgaggctgg tagtgactgg 1260
atggacacat tgctgtgggt agtccctcct actaggaggc ttgtcatact gtctagaggt 1320
tgactcttag ttctgtaaat aaagacatcc atttcaaaca gccaaaa 1367

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&lt;210&gt; 108

&lt;211&gt; 413

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 108

```

Asp Thr Gly Leu Glu Ala Val Ser Asp Lys Cys Ser Gln Glu Val Gly
1          5          10          15
Thr Pro Leu Arg Glu Glu Arg Gly Ala Thr Gly Leu Gly Pro Val Ile
20          25          30
Ala Met Gly Ser Gly Cys Arg Ile Glu Cys Ile Phe Phe Ser Glu Phe
35          40          45
His Pro Thr Leu Gly Pro Lys Ile Thr Tyr Gln Val Pro Glu Asp Phe
50          55          60
Ile Ser Arg Glu Leu Phe Asp Thr Val Gln Val Tyr Ile Ile Thr Lys
65          70          75          80
Pro Glu Leu Gln Asn Lys Leu Ile Thr Val Thr Ala Met Glu Lys Lys
85          90          95
Leu Ile Gly Cys Pro Val Cys Ile Glu His Lys Lys Tyr Ser Arg Asn
100          105          110
Ala Leu Leu Phe Asn Leu Gly Phe Val Cys Asp Ala Gln Ala Lys Thr
115          120          125
Cys Ala Leu Glu Pro Ile Val Lys Lys Leu Ala Gly Tyr Leu Thr Thr
130          135          140
Leu Glu Leu Glu Ser Ser Phe Val Ser Met Glu Glu Ser Lys Gln Lys
145          150          155          160
Leu Val Pro Ile Met Thr Ile Leu Leu Glu Glu Leu Asn Ala Ser Gly
165          170          175
Arg Cys Thr Leu Pro Ile Asp Glu Ser Asn Thr Ile His Leu Lys Val
180          185          190
Ile Glu Gln Arg Pro Asp Pro Pro Val Ala Gln Glu Tyr Asp Val Pro
195          200          205
Val Phe Thr Lys Asp Lys Glu Asp Phe Phe Asn Ser Gln Trp Asp Leu
210          215          220
Thr Thr Gln Gln Ile Leu Pro Tyr Ile Asp Gly Phe Arg His Ile Gln
225          230          235          240
Lys Ile Ser Ala Glu Ala Asp Val Glu Leu Asn Leu Val Arg Ile Ala
245          250          255
Ile Gln Asn Leu Leu Tyr Tyr Gly Val Val Thr Leu Val Ser Ile Leu
260          265          270
Gln Tyr Ser Asn Val Tyr Cys Pro Thr Pro Lys Val Gln Asp Leu Val

```

275	280	285
Asp Asp Lys Ser Leu Gln Glu Ala Cys Leu Ser Tyr Val Thr Lys Gln		
290	295	300
Gly His Lys Arg Ala Ser Leu Arg Asp Val Phe Gln Leu Tyr Cys Ser		
305	310	315
Leu Ser Pro Gly Thr Thr Val Arg Asp Leu Ile Gly Arg His Pro Gln		
325	330	335
Gln Leu Gln His Val Asp Glu Arg Lys Leu Ile Gln Phe Gly Leu Met		
340	345	350
Lys Asn Leu Ile Arg Arg Leu Gln Lys Tyr Pro Val Arg Val Thr Arg		
355	360	365
Glu Glu Gln Ser His Pro Ala Arg Leu Tyr Thr Gly Cys His Ser Tyr		
370	375	380
Asp Glu Ile Cys Cys Lys Thr Gly Met Ser Tyr His Glu Leu Asp Glu		
385	390	395
Arg Leu Glu Asn Asp Pro Asn Ile Ile Ile Cys Trp Lys		
405	410	

<210> 109  
 <211> 2113  
 <212> DNA  
 <213> Homo Sapiens

<400> 109

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ctatggagca	ggtcaatgag	ctgaaggaga	aaggcaacaa	ggccctgagc	gtgggtaaca	120
tcgatgatgc	cttacagtgc	tactccgaag	ctattaagct	ggatccccac	aaccacgtgc	180
tgtacagcaa	cgtttctgct	gcctatgcca	agaaaggaga	ctaccagaag	gcttatgagg	240
atggctgcaa	gactgtcgac	ctaaagcctg	actggggcaa	gggctattca	cgaaaagcag	300
cagctctaga	gtttcttaaac	cgctttgaag	aagccaagcg	aacctatgag	gagggcttaa	360
aacacgaggc	aaataaccct	caactgaaag	agggtttaca	gaatatggag	gccagggttg	420
cagagagaaa	attcatgaac	cctttcaaca	tgcctaattc	gtatcagaag	ttggagagtg	480
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gaaacaagcc	ttctgacctg	ggcacgaaac	tacaagatcc	ccggatcatg	accactctca	600
gcgtctctct	tggggctcgat	ctgggcagta	tggatgagga	ggaagagatt	gcaacacctc	660
caccaccacc	ccctcccaaa	aaggagacca	agccagagcc	aatggaagaa	gatcttccag	720
agaataagaa	gcaggcactg	aaagaaaaag	agctggggaa	cgatgcctac	aagaagaaag	780
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ctttggagga	gaagaacaaa	ggcaacgagt	gttttcagaa	aggggactat	cccaggcca	1200
tgaagcatta	tacagaagcc	atcaaaagga	acccgaaaga	tgccaaatta	tacagcaatc	1260
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gtatccagct	ggagccgacc	ttcatcaagg	gttatacacg	gaaagccgct	gcgctggaag	1380
cgatgaagga	ctacaccaa	gccatggatg	tgtaccagaa	ggcgctagac	ctggactcca	1440
gctgtaagga	ggcggcagac	ggctaccagc	gctgtatgat	ggcgagctac	aaccggcacg	1500
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aacacttaaa	gaatcctgta	atagcacaga	agatccagaa	gctgatggat	gtgggtctga	1680
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gctgggaccg	cggcgagcag	cacggagcgg	aagggagagc	aggggagaga	aggcctcatc	1800
tctctatatt	tatacataac	cccggggaag	acacagagac	tcttacctgc	gctgtttgtg	1860

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ccgccgctgc ctctgggccc tcccagcaca cgcattggtct cttcaccgct gccctcgagt 1920
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ttttttatatt ggggcagtgg gcatgttatg gggaggggag ggggttcttc cagcctcagg 2040
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gcgtggttat aac 2113

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&lt;210&gt; 110

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 110

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Met Glu Gln Val Asn Glu Leu Lys Glu Lys Gly Asn Lys Ala Leu Ser
 1          5          10          15
Val Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile Lys
 20          25          30
Leu Asp Pro His Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala Tyr
 35          40          45
Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr
 50          55          60
Val Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala Ala
 65          70          75          80
Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu
 85          90          95
Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly Leu
100          105          110
Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe
115          120          125
Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr Arg
130          135          140
Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Arg
145          150          155          160
Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile Met
165          170          175
Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu
180          185          190
Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Pro Lys Lys Glu
195          200          205
Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln
210          215          220
Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp
225          230          235          240
Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp Pro
245          250          255
Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu Lys
260          265          270
Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val
275          280          285
Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala
290          295          300
Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile
305          310          315          320
His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu
325          330          335
Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu

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340	345	350
Ala Tyr Ile Asn Pro Asp Leu	Ala Leu Glu Glu Lys Asn Lys Gly Asn	
355	360	365
Glu Cys Phe Gln Lys Gly Asp Tyr	Pro Gln Ala Met Lys His Tyr Thr	
370	375	380
Glu Ala Ile Lys Arg Asn Pro Lys	Asp Ala Lys Leu Tyr Ser Asn Arg	
385	390	395
Ala Ala Cys Tyr Thr Lys Leu Leu	Glu Phe Gln Leu Ala Leu Lys Asp	400
405	410	415
Cys Glu Glu Cys Ile Gln Leu Glu	Pro Thr Phe Ile Lys Gly Tyr Thr	
420	425	430
Arg Lys Ala Ala Ala Leu Glu Ala	Met Lys Asp Tyr Thr Lys Ala Met	
435	440	445
Asp Val Tyr Gln Lys Ala Leu Asp	Leu Asp Ser Ser Cys Lys Glu Ala	
450	455	460
Ala Asp Gly Tyr Gln Arg Cys Met	Met Ala Gln Tyr Asn Arg His Asp	
465	470	475
Ser Pro Glu Asp Val Lys Arg Arg	Ala Met Ala Asp Pro Glu Val Gln	
485	490	495
Gln Ile Met Ser Asp Pro Ala Met	Arg Leu Ile Leu Glu Gln Met Gln	
500	505	510
Lys Asp Pro Gln Ala Leu Ser Glu	His Leu Lys Asn Pro Val Ile Ala	
515	520	525
Gln Lys Ile Gln Lys Leu Met Asp	Val Gly Leu Ile Ala Ile Arg	
530	535	540

<210> 111  
 <211> 2765  
 <212> DNA  
 <213> Homo Sapiens

<400> 111

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caaccaccg	ctgccgaaat	gaagtataag	aatcttatgg	caagggcctt	atatgacaat	180
gtcccagagt	gtgccgagga	actggccttt	cgcaagggag	acatcctgac	cgatcatagag	240
cagaacacag	ggggactgga	aggatggtgg	ctgtgtctcg	tacacggtcg	gcaaggcatt	300
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gagcagcctg	cctctggact	gatgcagcag	acctttggcc	aacagaagct	ctatcaagtg	420
ccaaaccac	aggctgctcc	ccgagacacc	atctaccaag	tgccaccttc	ctaccaaaat	480
caggaatttt	accaagtccc	cactggccac	ggcaccacaag	aacaagaggt	atatcagggtg	540
ccaccatcag	tgcagagaag	cattggggga	accagtgggc	cccacgtggg	taaaaagggtg	600
ataacccccg	tgaggacagg	ccatggctac	gtatacgagt	acccatccag	ataccaaaaag	660
gatgtctatg	atatacctcc	ttctcatacc	actcaagggg	tatacgacat	ccctccctca	720
tcagcaaaaag	gccctgtgtt	ttcagttcca	gtgggagaga	taaaacctca	aggggtgtat	780
gacatccccg	ctacaaaagg	ggtatatgcc	attccgccct	ctgcttgccg	ggatgaagca	840
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gctaaaggct	ctcgggactt	ggtggatggg	atcaaccgat	tgtctttctc	cagtacaggc	1260
agcaccggga	gtaacatgtc	cagtccttcc	acctcctcca	aggagtccctc	actgtcagcc	1320
tccccagctc	aggacaaaag	gctcttctctg	gatccagaca	cagctattga	gagacttcag	1380

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gtggagctgt tcctgaagga gtacctccac ttgtcaagg gagctgttgc aaatgctgcc 1560
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tcccaccaga tcctgagtca aaccagccat gacttaaata agtcgagctg gtccctgaat 1680
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gccctcttca gaccgggcc tggcagcttg catctgaaga atgggcccga gagcatcatg 1860
aactcaacgg agtaccacac cgggtggctcc cagggacagc tgctgcatcc tggtgaccac 1920
aaggcccagg ccacacaaca ggcaactgcc ccaggcctga gcaaggagca ggcccctgac 1980
tgtagcagca gtgatggttc tgagaggagc tggatggatg actacgatta cgtccaccta 2040
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aaacagaaca agatgcagct ggaacatcat cagctgagcc agttccagct gttggaacaa 2160
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&lt;210&gt; 112

&lt;211&gt; 834

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 112

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Met Lys Tyr Lys Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro
 1             5             10             15
Glu Cys Ala Glu Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val
             20             25             30
Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu
             35             40             45
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile
             50             55             60
Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly
65             70             75             80
Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn
             85             90             95
Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr
             100            105            110
Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu
             115            120            125
Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly
             130            135            140
Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr
145            150            155            160
Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val
             165            170            175
Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro
             180            185            190

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Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile  
 195 200 205  
 Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala  
 210 215 220  
 Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp  
 225 230 235 240  
 Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg  
 245 250 255  
 Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly  
 260 265 270  
 Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu  
 275 280 285  
 Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro  
 290 295 300  
 Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro  
 305 310 315 320  
 Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala  
 325 330 335  
 Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro  
 340 345 350  
 Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu  
 355 360 365  
 Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser  
 370 375 380  
 Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys  
 385 390 395 400  
 Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu  
 405 410 415  
 Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr  
 420 425 430  
 Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile  
 435 440 445  
 Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His  
 450 455 460  
 Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile  
 465 470 475 480  
 Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His  
 485 490 495  
 Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser  
 500 505 510  
 Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu  
 515 520 525  
 Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln  
 530 535 540  
 Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly  
 545 550 555 560  
 Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser  
 565 570 575  
 Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly  
 580 585 590  
 Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser  
 595 600 605  
 Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser  
 610 615 620  
 Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe

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<210> 113
<211> 3429
<212> DNA
<213> Homo Sapiens
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<400> 113							
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cttgtaaaca	ccaatagtaa	agggccctct	aataagaaga	gaggtcgttc	taagaaggcc		240
catgttttgg	ctgcatctgt	tgaacaagca	actgagaatt	tcttgagaa	gggggataaa		300
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gaaagaagtg	atgcactcaa	ttctgcaata	gataaaatga	ccaagaagac	cagggacttg		1200
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attactaatg tacgctgctg caggacatta ataaagttgc ttttttaggc tacagtgtct 3420
cgatgccat 3429

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&lt;210&gt; 114

&lt;211&gt; 906

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 114

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Met Thr Ala Val His Ala Gly Asn Ile Asn Phe Lys Trp Asp Pro Lys
1          5          10          15
Ser Leu Glu Ile Arg Thr Leu Ala Val Glu Arg Leu Leu Glu Pro Leu
20          25          30
Val Thr Gln Val Thr Thr Leu Val Asn Thr Asn Ser Lys Gly Pro Ser
35          40          45
Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
50          55          60
Val Glu Gln Ala Thr Glu Asn Phe Leu Glu Lys Gly Asp Lys Ile Ala
65          70          80
Lys Glu Ser Gln Phe Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp

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	85		90		95
Val Arg Lys Gln Gly Asp Leu Met Lys Ala Ala Ala Gly Glu Phe Ala					
	100		105		110
Asp Asp Pro Cys Ser Ser Val Lys Arg Gly Asn Met Val Arg Ala Ala					
	115		120		125
Arg Ala Leu Leu Ser Ala Val Thr Arg Leu Leu Ile Leu Ala Asp Met					
	130		135		140
Ala Asp Val Tyr Lys Leu Leu Val Gln Leu Lys Val Val Glu Asp Gly					
145		150		155	160
Ile Leu Lys Leu Arg Asn Ala Gly Asn Glu Gln Asp Leu Gly Ile Gln					
	165		170		175
Tyr Lys Ala Leu Lys Pro Glu Val Asp Lys Leu Asn Ile Met Ala Ala					
	180		185		190
Lys Arg Gln Gln Glu Leu Lys Asp Val Gly His Arg Asp Gln Met Ala					
	195		200		205
Ala Ala Arg Gly Ile Leu Gln Lys Asn Val Pro Ile Leu Tyr Thr Ala					
	210		215		220
Ser Gln Ala Cys Leu Gln His Pro Asp Val Ala Ala Tyr Lys Ala Asn					
225		230		235	240
Arg Asp Leu Ile Tyr Lys Gln Leu Gln Gln Ala Val Thr Gly Ile Ser					
	245		250		255
Asn Ala Ala Gln Ala Thr Ala Ser Asp Ala Ser Gln His Gln Gly					
	260		265		270
Gly Gly Gly Gly Glu Leu Ala Tyr Ala Leu Asn Asn Phe Asp Lys Gln					
	275		280		285
Ile Ile Val Asp Pro Leu Ser Phe Ser Glu Glu Arg Phe Arg Pro Ser					
	290		295		300
Leu Glu Glu Arg Leu Glu Ser Ile Ile Ser Gly Ala Ala Leu Met Ala					
305		310		315	320
Asp Ser Ser Cys Thr Arg Asp Asp Arg Arg Glu Arg Ile Val Ala Glu					
	325		330		335
Cys Asn Ala Val Arg Gln Ala Leu Gln Asp Leu Leu Ser Glu Tyr Met					
	340		345		350
Gly Asn Ala Gly Arg Lys Glu Arg Ser Asp Ala Leu Asn Ser Ala Ile					
	355		360		365
Asp Lys Met Thr Lys Lys Thr Arg Asp Leu Arg Arg Gln Leu Arg Lys					
	370		375		380
Ala Val Met Asp His Val Ser Asp Ser Phe Leu Glu Thr Asn Val Pro					
385		390		395	400
Leu Leu Val Leu Ile Glu Ala Ala Lys Asn Gly Asn Glu Lys Glu Val					
	405		410		415
Lys Glu Tyr Ala Gln Val Phe Arg Glu His Ala Asn Lys Leu Ile Glu					
	420		425		430
Val Ala Asn Leu Ala Cys Ser Ile Ser Asn Asn Glu Glu Gly Val Lys					
	435		440		445
Leu Val Arg Met Ser Ala Ser Gln Leu Glu Ala Leu Cys Pro Gln Val					
	450		455		460
Ile Asn Ala Ala Leu Ala Leu Ala Ala Lys Pro Gln Ser Lys Leu Ala					
465		470		475	480
Gln Glu Asn Met Asp Leu Phe Lys Glu Gln Trp Glu Lys Gln Val Arg					
	485		490		495
Val Leu Thr Asp Ala Val Asp Asp Ile Thr Ser Ile Asp Asp Phe Leu					
	500		505		510
Ala Val Ser Glu Asn His Ile Leu Glu Asp Val Asn Lys Cys Val Ile					
	515		520		525

Ala Leu Gln Glu Lys Asp Val Asp Gly Leu Asp Arg Thr Ala Gly Ala  
 530 535 540  
 Ile Arg Gly Arg Ala Ala Arg Val Ile His Val Val Thr Ser Glu Met  
 545 550 555 560  
 Asp Asn Tyr Glu Pro Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr  
 565 570 575  
 Lys Leu Leu Ser Asn Thr Val Met Pro Arg Phe Thr Glu Gln Val Glu  
 580 585 590  
 Ala Ala Val Glu Ala Leu Ser Ser Asp Pro Ala Gln Pro Met Asp Glu  
 595 600 605  
 Asn Glu Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Ile Arg Asp  
 610 615 620  
 Ile Arg Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Asp Asp  
 625 630 635 640  
 Ser Asp Phe Glu Thr Glu Asp Phe Asp Val Arg Ser Arg Thr Ser Val  
 645 650 655  
 Gln Thr Glu Asp Asp Gln Leu Ile Ala Gly Gln Ser Ala Arg Ala Ile  
 660 665 670  
 Met Ala Gln Leu Pro Gln Glu Gln Lys Ala Lys Ile Ala Glu Gln Val  
 675 680 685  
 Ala Ser Phe Gln Glu Glu Lys Ser Lys Leu Asp Ala Glu Val Ser Lys  
 690 695 700  
 Trp Asp Asp Ser Gly Asn Asp Ile Ile Val Leu Ala Lys Gln Met Cys  
 705 710 715 720  
 Met Ile Met Met Glu Met Thr Asp Phe Thr Arg Gly Lys Gly Pro Leu  
 725 730 735  
 Lys Asn Thr Ser Asp Val Ile Ser Ala Ala Lys Lys Ile Ala Glu Ala  
 740 745 750  
 Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro  
 755 760 765  
 Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala  
 770 775 780  
 Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val  
 785 790 795 800  
 Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met  
 805 810 815  
 Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr  
 820 825 830  
 Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly  
 835 840 845  
 Met Ala Ser Leu Asn Leu Pro Ala Val Ser Trp Lys Met Lys Ala Pro  
 850 855 860  
 Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr  
 865 870 875 880  
 Lys Ile Lys Arg Ala Ser Gln Lys Lys His Val Asn Pro Val Gln Ala  
 885 890 895  
 Leu Ser Glu Phe Lys Ala Met Asp Ser Ile  
 900 905

&lt;210&gt; 115

&lt;211&gt; 1701

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 115

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cggccggccg ccatggctaa cgtggctgac acgaagctgt acgacatcct gggcggtccc      60
gcggggcgcca gcgagaacga gctgaagaag gcatacagaa agttagccaa ggaatatcat      120
cctgataaga atccccc aaat gcaggagaca aactttaaag aaataagttt tgcatatgaa      180
gtactatcaa atcctgagaa gcgtgagtta tatgacagat acggagagca aggtcttcgg      240
gaaggcagcg gcggaggtgg gtggcatgga ttgatatttt ctctcaccgt tttttgtggg      300
ggattgttcg gcttcatggg caatcagagt agaagtcgaa atggcagaag aagaggagag      360
gacatgatgc atccactcaa agtatcttta gaagatctgt ataatggcaa gacaaccaa      420
ctacaactta gcaagaatgt gctctgtagt gcatgcagtg gccaaaggcg aaagtctgga      480
gctgtccaaa agtgtagtgc ttgtcgaggt cgaggtgtgc gcatcatgat cagacagctg      540
gctccaggga tggtaacaac gatgcagttc gtgtgctctg attgtaatgg tgaaggagag      600
gtaattaatg aaaaagaccg ctgtaaaaaa tgtgaaggga agaaggtgat taaagaagtc      660
aagattcttg aagtccacgt agacaaaggc atgaaacatg gacagagaat tacattcact      720
ggggaagcag accaggcccc agagtggaaac ccggagacat tgttcttttt gctaccagga      780
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ggacttggtg aagctctatg tggatttcag ttcacattaa gccaccttga tggacgtcag      900
atttgtgtga aatacccccc tggcaaagta attgaaccag ggtgtgttcg tgtagtctga      960
ggtgaaggga tgccgcagta tcgtaatccc tttgaaaaag gtgggcttta cataaagttt     1020
gatgtgcagt ttcctgaaaa caactggatc aaccagaca agctttctga actagaagat     1080
cttctgccat ctagaccgga agttcctaac ataattggag aaacagagga ggtagagctt     1140
caggaatttg atagactcg aggtcagga ggtggtcaga ggcgtgaagc ctataatgat     1200
agctctgatg aagaaagcag cagccatcat ggacctggag tgcagtgtgc ccatacagtaa     1260
actctgcaaa caaattgcac aggtggattt tctttccaca tttgcctgat ttgttctcag     1320
caatccagct ggagtgtctt atcaatccag atgaaactgag ggacatctgt tggctctatgt     1380
ataactttta aaattgggat agtatctaca gagtgtataa tttaaactaa ccacaaagct     1440
ttacatttcc attttgactg ttccatagca gaataaagca cttgaaagga aacaagactc     1500
cctttcacac atggattatt ataagtttca atcctggtat ctgtgcttga tttttatcag     1560
ttttgtgtag atttttatgt ttcatatatt aaatttaaat ccacattgt aaagtttgta     1620
caatttgtcc tgaagctttg tgtttggctg cacctgcata agctgctaca aatagaataa     1680
agaatttcat agcctgtaaa a                                     1701

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&lt;210&gt; 116

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 116

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Met Ala Asn Val Ala Asp Thr Lys Leu Tyr Asp Ile Leu Gly Val Pro
 1              5              10              15
Ala Gly Ala Ser Glu Asn Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala
 20              25              30
Lys Glu Tyr His Pro Asp Lys Asn Pro Gln Met Gln Glu Thr Asn Phe
 35              40              45
Lys Glu Ile Ser Phe Ala Tyr Glu Val Leu Ser Asn Pro Glu Lys Arg
 50              55              60
Glu Leu Tyr Asp Arg Tyr Gly Glu Gln Gly Leu Arg Glu Gly Ser Gly
 65              70              75              80
Gly Gly Gly Trp His Gly Leu Ile Phe Ser Leu Thr Val Phe Cys Gly
 85              90              95
Gly Leu Phe Gly Phe Met Gly Asn Gln Ser Arg Ser Arg Asn Gly Arg
100              105              110
Arg Arg Gly Glu Asp Met Met His Pro Leu Lys Val Ser Leu Glu Asp
115              120              125
Leu Tyr Asn Gly Lys Thr Thr Lys Leu Gln Leu Ser Lys Asn Val Leu
130              135              140
Cys Ser Ala Cys Ser Gly Gln Gly Gly Lys Gly Ala Val Gln Lys

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145		150		155		160
Cys Ser Ala Cys Arg Gly Arg Gly Val Arg Ile Met Ile Arg Gln Leu						
	165		170			175
Ala Pro Gly Met Val Gln Gln Met Gln Ser Val Cys Ser Asp Cys Asn						
	180		185			190
Gly Glu Gly Glu Val Ile Asn Glu Lys Asp Arg Cys Lys Lys Cys Glu						
	195		200			205
Gly Lys Lys Val Ile Lys Glu Val Lys Ile Leu Glu Val His Val Asp						
	210		215			220
Lys Gly Met Lys His Gly Gln Arg Ile Thr Phe Thr Gly Glu Ala Asp						
225		230		235		240
Gln Ala Pro Glu Trp Asn Pro Glu Thr Leu Phe Phe Leu Leu Pro Gly						
	245		250			255
Glu Lys Asn Met Glu Val Phe Gln Arg Asp Gly Asn Asp Leu His Met						
	260		265			270
Thr Tyr Lys Ile Gly Leu Val Glu Ala Leu Cys Gly Phe Gln Phe Thr						
	275		280			285
Leu Ser His Leu Asp Gly Arg Gln Ile Val Val Lys Tyr Pro Pro Gly						
	290		295			300
Lys Val Ile Glu Pro Gly Cys Val Arg Val Val Arg Gly Glu Gly Met						
305		310		315		320
Pro Gln Tyr Arg Asn Pro Phe Glu Lys Gly Gly Leu Tyr Ile Lys Phe						
	325		330			335
Asp Val Gln Phe Pro Glu Asn Asn Trp Ile Asn Pro Asp Lys Leu Ser						
	340		345			350
Glu Leu Glu Asp Leu Leu Pro Ser Arg Pro Glu Val Pro Asn Ile Ile						
	355		360			365
Gly Glu Thr Glu Glu Val Glu Leu Gln Glu Phe Asp Ser Thr Arg Gly						
	370		375			380
Ser Gly Gly Gly Gln Arg Arg Glu Ala Tyr Asn Asp Ser Ser Asp Glu						
385		390		395		400
Glu Ser Ser Ser His His Gly Pro Gly Val Gln Cys Ala His Gln						
	405		410			415

&lt;210&gt; 117

&lt;211&gt; 1821

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 117

cgcggtgaact gcttcctgca ggctggccat ggcgcttcac gttcccaagg ctccgggctt	60
tgcccagatg ctcaaggagg gagcgaaaca cttttcagga ttagaagagg ctgtgtatag	120
aaacatacaa gcttgcaagg agcttgccca aaccactcgt acagcatatg gaccaaagg	180
aatgaacaaa atggttatca accacttgga gaagttgttt gtgacaaacg atgcagcaac	240
tattttaaga gaactagaag tacagcatcc tgctgcaaaa atgattgtaa tggcttctca	300
tatgcaagag caagaagttg gagatggcac aaactttgtt ctggtatttg ctggagctct	360
cctggaatta gctgaagaac ttctgaggat tggcctgtca gtttcagagg tcatagaagg	420
ttatgaaata gctgcagaa aagctcatga gattcttcct aatttggtat gttgttctgc	480
aaaaaacctt cgagatatgt atgaagtctc atctctactt cgtacctcca taatgagtaa	540
acaatatggt aatgaagtat ttctggccaa gcttattgct caggcatgcg tatctatatt	600
tcctgattcc ggccatttca atgttgataa catcagagtt tgtaaaattc tgggctctgg	660
tatcagttcc tcttcagtat tgcattggcat gggttttaag aaggaaaccg aaggatgatg	720
aacatctgtc aaagatgcaa aaatagcagt gtactcttgt ccttttgatg gcatgataac	780
agaaactaag ggaacagtgt tgataaagac tgctgaagaa ttgatgaatt ttagtaaggg	840
agaagaaaac ctcatggatg cacaagtcaa agctattgct gatactggtg caaatgtcgt	900

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agtaacaggt ggcaaagtgg cagacatggc tcttcattat gcaaataaat ataatatcat      960
gtagtgagg ctaaactcaa aatgggatct ccgaagactt tgtaaaactg ttggtgctac      1020
agctcttctt agattgacac ctcctgtcct tgaagaaatg ggacactgtg acagtgttta      1080
cctctcagaa gttggagata ctcaggtggg ggtttttaag catgaaaagg aagatggcgc      1140
catttctacc atagtacttc gaggtcttac agacaatctg atggatgaca tagaaagggg      1200
agtagacgat ggtgtttaata ctttcaaagt tcttacaagg gataaacgtc ttgtaccggg      1260
aggtggagca acagaaattg aattagccaa acagatcaca tcatatggag agacatgtcc      1320
tggaacttgaa cagtatgcta ttaagaagtt tgctgaggca tttgaagcta ttccccgcgc      1380
actggcagaa aactctggag ttaaggccaa tgaagtaatc tctaaacttt atgcagtaca      1440
tcaagaagga aataaaaaacg ttggattaga tattgaggct gaagtccctg ctgtaaagga      1500
catgctggaa gctggtattc tagatactta cctgggaaaa tattgggcta tcaaactcgc      1560
tactaatgct gcagtcactg tacttagagt ggatcagatc atcatggcaa aaccagctgg      1620
tgggcccaag cctccaagtg ggaagaaaga ctgggatgat gaccaaagt attgaaattg      1680
gcttaatttt tactgtaggt gaaggctgta tttgtagtag tactcaagaa tcacctgatg      1740
ttttcttatt ctccttaaat taagagttat tttgtgtttg tattcttggc tggatgttat      1800
aataaacata ttgttactgt c                                     1821

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&lt;210&gt; 118

&lt;211&gt; 548

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 118

```

Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
 1              5              10              15
Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
      20              25              30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
      35              40              45
Pro Lys Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
      50              55              60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
      65              70              75              80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
      85              90              95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
      100              105              110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
      115              120              125
Ile Glu Gly Tyr Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro
      130              135              140
Asn Leu Val Cys Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val
      145              150              155              160
Ser Ser Leu Leu Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu
      165              170              175
Val Phe Leu Ala Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro
      180              185              190
Asp Ser Gly His Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu
      195              200              205
Gly Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys
      210              215              220
Lys Glu Thr Glu Gly Asp Val Thr Ser Val Lys Asp Ala Lys Ile Ala
      225              230              235              240
Val Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr
      245              250              255

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Val Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu  
 260 265 270  
 Glu Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala  
 275 280 285  
 Asn Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr  
 290 295 300  
 Ala Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp  
 305 310 315 320  
 Leu Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu  
 325 330 335  
 Thr Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu  
 340 345 350  
 Ser Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu  
 355 360 365  
 Asp Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu  
 370 375 380  
 Met Asp Asp Ile Glu Arg Val Val Asp Asp Gly Val Asn Thr Phe Lys  
 385 390 395 400  
 Val Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu  
 405 410 415  
 Ile Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly  
 420 425 430  
 Leu Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile  
 435 440 445  
 Pro Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile  
 450 455 460  
 Ser Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu  
 465 470 475 480  
 Asp Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly  
 485 490 495  
 Ile Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr  
 500 505 510  
 Asn Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys  
 515 520 525  
 Pro Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp  
 530 535 540  
 Asp Gln Asn Asp  
 545

&lt;210&gt; 119

&lt;211&gt; 1321

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 119

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cccccaagat ggctgctgag gacgagttac agctgccgcg gctccccgag ctgttcgaaa      60
ctggttagaca gttactggac gaagtagaag tggcgactga acccgccggt tccgggatag      120
tccaggagaa ggtgttcaag ggcttggacc tccttgagaa ggctgccgaa atgttatcgc      180
agctcgactt gttcagccga aatgaagatt tggaagagat tgcttcacc gacctgaagt      240
accttttggt gccagcgttt caaggagccc tcaccatgaa acaagtcaac cccagcaagc      300
gtctagatca tttgcagcgg gctcgagaac actttataaa ctacttaact cagtgccatt      360
gctatcatgt ggcagagttt gagctgcccc aaaccatgaa caactctgct gaaaatcaca      420
ctgccaatte ctccatggct taccctagtc tcgttgctat ggcattctcaa agacaggcta      480
aaatacagag atacaagcag aagaaggagt tggagcatag gttgtctgca atgaaatctg      540
ctgtggaaaag tggtaagca gatgatgagc gtgttcgtga atattatctt cttcaccttc      600
  
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agaggtggat tgatatcagc ttagaagaga ttgagagcat tgaccaggaa ataaagatcc 660
tgagagaaag agactcttca agagagggcat caacttctaa ctcattctgc caggagaggc 720
ctccagtga acccttcatt ctcaactcga acatggctca agccaaagta tttggagctg 780
gttatccaag tctgccaact atgacgggtga gtgactggta tgagcaacat cggaaatatg 840
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gctaaatctt gctttgcatt cagtaaagtg tcaagtgatt aagtgtgtat ttgtacccta 1200
gatgatatga accagcagtc ttgttttggc atcactctca tcatgttgta ttccagcttc 1260
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c 1321

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<210> 120  
 <211> 339  
 <212> PRT  
 <213> Homo Sapiens

<400> 120

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Met Ala Ala Glu Asp Glu Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe
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20     25     30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
35     40     45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
50     55     60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
65     70     75     80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
85     90     95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
100    105    110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
115    120    125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
130    135    140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
145    150    155    160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
165    170    175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
180    185    190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
195    200    205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
210    215    220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
225    230    235    240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
245    250    255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
260    265    270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala

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275	280	285
Ala Pro Glu Glu Phe Arg Lys Ala Ala Gln Gln Gln Glu Glu Gln Glu		
290	295	300
Glu Lys Glu Glu Glu Asp Asp Glu Gln Thr Leu His Arg Ala Arg Glu		
305	310	315
Trp Asp Asp Trp Lys Asp Thr His Pro Arg Gly Tyr Gly Asn Arg Gln		
325	330	335
Asn Met Gly		

<210> 121  
 <211> 2965  
 <212> DNA  
 <213> Homo Sapiens

<400> 121

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tgagcccgcg	ggagcccagg	acgccgcttc	cccgcccatc	cccgtcctcc	gaggccggcc	180
gcctgggtcat	ggcgcagccg	ggcccggctt	cccagcctga	cgtttctctt	cagcaacggg	240
tagcagaatt	ggaaaaaatt	aatgcagaat	ttttacgtgc	acaacagcag	cttgaacaag	300
aatttaatca	aaagagagca	aaatttaagg	agttatat	ggctaaagag	gaggatctga	360
agaggcaaaa	tcaggtatta	caagctgcac	aagatgattt	gggacacctt	cgaaccagc	420
tgtgggaagc	tcaagcagag	atggagaata	ttaaggcgat	tgccacagtc	tctgagaaca	480
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gaagaaggct	gtctgaagg	caagaggagg	aaaatttaga	aaatgaaatg	aaaaaggccc	720
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aagaactgaa	tcattatctg	gaagctgaga	aatctttag	gactgatcta	gagatgtatg	900
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aaaaactaca	gctgatgcta	aggcaagcta	atgaccagtt	agagaagaca	atgaaagata	1920
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gtttaaaaga aaatcttgaa gaaactctgc aactagaaat agaaaactgc aaggaggaaa 2400
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caaaaggaag actggagaaa tgcttacttc tagagggaga agactgtgcg gcacaggaaa 2940
cagcaaacag tggggtgacg tgcag 2965

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&lt;210&gt; 122

&lt;211&gt; 862

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 122

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Met Ala Gln Pro Gly Pro Ala Ser Gln Pro Asp Val Ser Leu Gln Gln
 1          5          10          15
Arg Val Ala Glu Leu Glu Lys Ile Asn Ala Glu Phe Leu Arg Ala Gln
 20          25          30
Gln Gln Leu Glu Gln Glu Phe Asn Gln Lys Arg Ala Lys Phe Lys Glu
 35          40          45
Leu Tyr Leu Ala Lys Glu Glu Asp Leu Lys Arg Gln Asn Ala Val Leu
 50          55          60
Gln Ala Ala Gln Asp Asp Leu Gly His Leu Arg Thr Gln Leu Trp Glu
 65          70          75          80
Ala Gln Ala Glu Met Glu Asn Ile Lys Ala Ile Ala Thr Val Ser Glu
 85          90          95
Asn Thr Lys Gln Glu Ala Ile Asp Glu Val Lys Arg Gln Trp Arg Glu
100          105          110
Glu Val Ala Ser Leu Gln Ala Val Met Lys Glu Thr Val Arg Asp Tyr
115          120          125
Glu His Gln Phe His Leu Arg Leu Glu Gln Glu Arg Thr Gln Trp Ala
130          135          140
Gln Tyr Arg Glu Tyr Ala Glu Arg Glu Ile Ala Asp Leu Arg Arg Arg
145          150          155          160
Leu Ser Glu Gly Gln Glu Glu Asn Leu Glu Asn Glu Met Lys Lys
165          170          175
Ala Gln Glu Asp Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu
180          185          190
Lys Glu Ile Ala Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys
195          200          205
Ile Lys Glu Leu Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu
210          215          220
Glu Ala Glu Lys Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val
225          230          235          240
Leu Asn Thr Gln Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg
245          250          255
Lys Glu Leu His Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln
260          265          270
His Asn Gln Leu Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu
275          280          285
Glu Ser Gln Arg Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val

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290		295		300
Leu Thr Ser Glu Gln	Leu Arg Gln Val Glu	Glu Leu Lys Lys Lys Asp		
305	310	315		320
Gln Glu Asp Asp Glu	Gln Gln Arg Leu Asn	Lys Arg Lys Asp His Lys		
	325	330		335
Lys Ala Asp Val Glu	Glu Glu Ile Lys Ile	Pro Val Val Cys Ala Leu		
	340	345		350
Thr Gln Glu Glu Ser	Ser Ala Gln Leu Ser	Asn Glu Glu Glu His Leu		
	355	360		365
Asp Ser Thr Arg Gly	Ser Val His Ser Leu	Asp Ala Gly Leu Leu Leu		
	370	375		380
Pro Ser Gly Asp Pro	Phe Ser Lys Ser Asp	Asn Asp Met Phe Lys Asp		
385	390	395		400
Gly Leu Arg Arg Ala	Gln Ser Thr Asp Ser	Leu Gly Thr Ser Gly Ser		
	405	410		415
Leu Gln Ser Lys Ala	Leu Gly Tyr Asn Tyr	Lys Ala Lys Ser Ala Gly		
	420	425		430
Asn Leu Asp Glu Ser	Asp Phe Gly Pro Leu	Val Gly Ala Asp Ser Val		
	435	440		445
Ser Glu Asn Phe Asp	Thr Ala Ser Leu Gly	Ser Leu Gln Met Pro Ser		
	450	455		460
Gly Phe Met Leu Thr	Lys Asp Gln Glu Arg	Ala Ile Lys Ala Met Thr		
465	470	475		480
Pro Glu Gln Glu Glu	Thr Ala Ser Leu Leu	Ser Ser Val Thr Gln Gly		
	485	490		495
Met Glu Ser Ala Tyr	Val Ser Pro Ser Gly	Tyr Arg Leu Val Ser Glu		
	500	505		510
Thr Glu Trp Asn Leu	Leu Gln Lys Glu Val	His Asn Ala Gly Asn Lys		
	515	520		525
Leu Gly Arg Arg Cys	Asp Met Cys Ser Asn	Tyr Glu Lys Gln Leu Gln		
	530	535		540
Gly Ile Gln Ile Gln	Glu Ala Glu Thr Arg	Asp Gln Val Lys Lys Leu		
545	550	555		560
Gln Leu Met Leu Arg	Gln Ala Asn Asp Gln	Leu Glu Lys Thr Met Lys		
	565	570		575
Asp Lys Gln Glu Leu	Glu Asp Phe Ile Lys	Gln Ser Ser Glu Asp Ser		
	580	585		590
Ser His Gln Ile Ser	Ala Leu Val Leu Arg	Ala Gln Ala Ser Glu Ile		
	595	600		605
Leu Leu Glu Glu Leu	Gln Gln Gly Leu Ser	Gln Ala Lys Arg Asp Val		
	610	615		620
Gln Glu Gln Met Ala	Val Leu Met Gln Ser	Arg Glu Gln Val Ser Glu		
625	630	635		640
Glu Leu Val Arg Leu	Gln Lys Asp Asn Asp	Ser Leu Gln Gly Lys His		
	645	650		655
Ser Leu His Val Ser	Leu Gln Gln Ala Glu	Asp Phe Ile Leu Pro Asp		
	660	665		670
Thr Thr Glu Ala Leu	Arg Glu Leu Val Leu	Lys Tyr Arg Glu Asp Ile		
	675	680		685
Ile Asn Val Arg Thr	Ala Ala Asp His Val	Glu Glu Lys Leu Lys Ala		
	690	695		700
Glu Ile Leu Phe Leu	Lys Glu Gln Ile Gln	Ala Glu Gln Cys Leu Lys		
705	710	715		720
Glu Asn Leu Glu Glu	Thr Leu Gln Leu Glu	Ile Glu Asn Cys Lys Glu		
	725	730		735

Glu Ile Ala Ser Ile Ser Ser Leu Lys Ala Glu Leu Glu Arg Ile Lys  
 740 745 750  
 Val Glu Lys Gly Gln Leu Glu Ser Thr Leu Arg Glu Lys Ser Gln Gln  
 755 760 765  
 Leu Glu Ser Leu Gln Glu Ile Lys Ile Ser Leu Glu Glu Gln Leu Lys  
 770 775 780  
 Lys Glu Thr Ala Ala Lys Ala Thr Val Glu Gln Leu Met Phe Glu Glu  
 785 790 795 800  
 Lys Asn Lys Ala Gln Arg Leu Gln Thr Glu Leu Asp Val Ser Glu Gln  
 805 810 815  
 Val Gln Arg Asp Phe Val Lys Leu Ser Gln Thr Leu Gln Val Gln Leu  
 820 825 830  
 Glu Arg Ile Arg Gln Ala Asp Ser Leu Glu Arg Ile Arg Ala Ile Leu  
 835 840 845  
 Asn Asp Thr Lys Leu Thr Asp Ile Asn Gln Leu Pro Glu Thr  
 850 855 860

<210> 123  
 <211> 544  
 <212> DNA  
 <213> Homo Sapiens

<400> 123  
 gggagtggcg tggcgcaggg atggcacaaa agaaatatct tcaagcaaaa ttgacccagt 60  
 ttttaaggga agacaggatt caactttgga aacctccata tacagatgaa aataaaaaag 120  
 ttggtttggc attaaaggac cttgctaagc agtactctga cagactagaa tgctgtgaaa 180  
 atgaagtata aaaggtaata gaagaaatac gttgcaaggc aattgagcgt ggaacaggaa 240  
 atgacaatta tagaacaacg ggaattgcta caatcgaggt gtttttacca ccaagactaa 300  
 aaaaagatag gaaaaacttg ttggagaccc gattgcacat cactggcaga gaactgaggt 360  
 ccaaaatagc tgaaaccttt ggacttcaag aanattatat caaaattgtc ataaataaga 420  
 agcaactacn actagggaaa acccttgaag ancaaggcgt ggctcacaat gtgaaagcga 480  
 tgggtgcttga actaaaacaa tctgaagagg acgcgaggaa aaacttccag ttagaggaag 540  
 agga 544

<210> 124  
 <211> 178  
 <212> PRT  
 <213> Homo Sapiens

<400> 124  
 Glu Trp Arg Gly Ala Gly Met Ala Gln Lys Lys Tyr Leu Gln Ala Lys  
 1 5 10 15  
 Leu Thr Gln Phe Leu Arg Glu Asp Arg Ile Gln Leu Trp Lys Pro Pro  
 20 25 30  
 Tyr Thr Asp Glu Asn Lys Lys Val Gly Leu Ala Leu Lys Asp Leu Ala  
 35 40 45  
 Lys Gln Tyr Ser Asp Arg Leu Glu Cys Cys Glu Asn Glu Val Glu Lys  
 50 55 60  
 Val Ile Glu Glu Ile Arg Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn  
 65 70 75 80  
 Asp Asn Tyr Arg Thr Thr Gly Ile Ala Thr Ile Glu Val Phe Leu Pro  
 85 90 95  
 Pro Arg Leu Lys Lys Asp Arg Lys Asn Leu Leu Glu Thr Arg Leu His  
 100 105 110  
 Ile Thr Gly Arg Glu Leu Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu



115 120 125  
 Gln Glu Tyr Ile Lys Ile Val Ile Asn Lys Lys Gln Leu Leu Gly Lys  
 130 135 140  
 Thr Leu Glu Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu  
 145 150 155 160  
 Leu Lys Gln Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu  
 165 170 175  
 Glu Glu

<210> 125  
 <211> 1302  
 <212> DNA  
 <213> Homo Sapiens

<400> 125  
 atggaggtgg tggacccgca gcagctgggc atgttcacgg agggcgagct gatgtcgggtg 60  
 ggtatggaca cgttcaccca ccgcatcgac tccaccgagg tcatctacca gccgcgccgc 120  
 aagcggggcca agctcatcgg caagtacctg atggggggacc tgctggggga aggtctttac 180  
 ggcaaggtga aggaggtgct ggactcggag acgctgtgca ggagggccgt caagatcctc 240  
 aagaagaaga agttgcgaag gatccccaac ggggaggcca acgtgaagaa ggaaattcaa 300  
 ctactgagga ggttacggca caaaaatgtc atccagctgg tggatgtgtt atacaacgaa 360  
 gagaagcaga aaatgtatat ggtgatggag tactgcgtgt gtggcatgca ggaaatgctg 420  
 gacagcgtgc cggagaagcg tttcccagtg tgccaggccc acgggtactt ctgtcagctg 480  
 attgacggcc tggagtacct gcatagccag ggcattgtgc acaaggacat caagccgggg 540  
 aacctgctgc tcaccaccgg tggcacccctc aaaatctccg acctgggctg ggccgaggca 600  
 ctgcaccctg tcgcggcgga cgacacctgc cggaccagcc agggctcccc ggctttccag 660  
 ccgcccagaga ttgccaacgg cctggacacc ttctccggct tcaaggtgga catctggctg 720  
 gctgggggtca ccctctacaa catcaccacg ggtctgtacc ccttcgaagg ggacaacatc 780  
 tacaagttgt ttgagaacat cgggaagggg agctacgcca tcccgggcga ctgtggcccc 840  
 ccgctctctg acctgctgaa agggatgctt gactacgaac cggccaagag gttctccatc 900  
 cggcagatcc ggcagcacag ctggttccgg aagaaacatc ctccggctga agcaccagtg 960  
 cccatcccac cgagcccaga caccaaggac cggtgggcgca gcatgactgt ggtgccgtac 1020  
 ttggaggacc tgcacggcgc ggacgaggac gaggacctct tcgacatcga ggatgacatc 1080  
 atctacactc aggacttcac ggtgcccgga cagggtcccag aagaggaggc cagtcacaat 1140  
 ggacagcgcc ggggcctccc caaggccgtg tgtatgaacg gcacagaggc ggccgagctg 1200  
 agcaccaaat ccagggcgga gggccgggcc cccaacctg cccgcaaggc ctgctccgcc 1260  
 agcagcaaga tccgcgggct gtcggcctgc aagcagcagt ga 1302

<210> 126  
 <211> 433  
 <212> PRT  
 <213> Homo Sapiens

<400> 126  
 Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu  
 1 5 10 15  
 Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr  
 20 25 30  
 Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys  
 35 40 45  
 Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys  
 50 55 60  
 Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu  
 65 70 75 80

Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys  
 85 90 95  
 Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Lys Asn Val Ile Gln  
 100 105 110  
 Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val  
 115 120 125  
 Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro  
 130 135 140  
 Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Cys Gln Leu  
 145 150 155 160  
 Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp  
 165 170 175  
 Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Gly Gly Thr Leu Lys Ile  
 180 185 190  
 Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Ala Asp Asp  
 195 200 205  
 Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile  
 210 215 220  
 Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser  
 225 230 235 240  
 Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu  
 245 250 255  
 Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser Tyr  
 260 265 270  
 Ala Ile Pro Gly Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Lys Gly  
 275 280 285  
 Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg  
 290 295 300  
 Gln His Ser Trp Phe Arg Lys Lys His Pro Pro Ala Glu Ala Pro Val  
 305 310 315 320  
 Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr  
 325 330 335  
 Val Val Pro Tyr Leu Glu Asp Leu His Gly Ala Asp Glu Asp Glu Asp  
 340 345 350  
 Leu Phe Asp Ile Glu Asp Asp Ile Ile Tyr Thr Gln Asp Phe Thr Val  
 355 360 365  
 Pro Gly Gln Val Pro Glu Glu Ala Ser His Asn Gly Gln Arg Arg  
 370 375 380  
 Gly Leu Pro Lys Ala Val Cys Met Asn Gly Thr Glu Ala Ala Gln Leu  
 385 390 395 400  
 Ser Thr Lys Ser Arg Ala Glu Gly Arg Ala Pro Asn Pro Ala Arg Lys  
 405 410 415  
 Ala Cys Ser Ala Ser Ser Lys Ile Arg Arg Leu Ser Ala Cys Lys Gln  
 420 425 430  
 Gln

&lt;210&gt; 127

&lt;211&gt; 1488

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 127

gaggggcccgg gcggtgccgg caagatggct ggcgccgaga agatgacgtt tcccagagaaa  
 ccaagccaca aaaagtacag ggccgccttg aagaaggaga aacgaaagaa acgtcggcag

60

120

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gaacttgctc gactgagaga ctcaggactc tcacagaagg aggaagagga ggacactttt 180
attgaagaac aacaactaga agaagagaag ctattggaaa gagagaggca aagattacat 240
gaggagtggg tgctaagaga gcagaaggca caagaagaat tcagaataaa gaaggaaaag 300
gaagagggcg ctaaaaaacg gcaagaagaa caagagagaa agttaagga acaatgggaa 360
gaacagcaga ggaaagagag agaagaggag gagcagaaac gacaggagaa gaaagaaaaa 420
gaggaagctt tgcagaagat gctggatcag gctgaaaatg agttggaaaa tggtaggaca 480
tggcaaaaacc cagaaccacc cgtggatttc agagtaatgg agaaggatcg agctaattgt 540
cccttctaca gtaaaacagg agcttgacga tttggagata gatgttcacg taaacataat 600
ttcccaacat ccagtcctac ctttcttatt aagagcatgt ttacgacgtt tggaaatggag 660
cagtgcagga gggatgacta tgaccctgac gcaagcctgg agtacagcga ggaagaaacc 720
taccaacagt tcctagactt ctatgaggat gtgttgcccg agttcaagaa cgtgggggaaa 780
gtgattcagt tcaaggtcag ctgcaatttg gaacctcacc tgagggggcaa tgtatatgtt 840
cagtaccagt cggaagaaga atgccaagca gccctttctc tgtttaacgg acgatggtat 900
gcaggacgac agctgcagtg tgaattctgc ccctgacccc ggtggaaaat ggcgatttgt 960
ggtttatattg aaatacaaca atgtccaaga ggaaagcact gcaactttct tcatgtgttc 1020
agaaatccca acaatgaatt ctgggaagct aatagagaca tctacttgct tccagatcgg 1080
actggctcct cctttgggaa gaactccgaa aggagggaga ggatgggcca ccacgacgac 1140
tactacagca ggctgcgggg aaggagaaac cctagtccag accactccta caaaagaaat 1200
ggggaatccg agaggaaaag tagtcgtcac agggggaaga aatctcacia acgcacatca 1260
aagagtcggg agaggcacia ttcacgaagc agaggaagaa atagggaccg cagcagggac 1320
cgcagccggg gccggggcag ccggagccgg agccggagcc ggagccgcag gagccgccgc 1380
agccggagcc aaagtctctc taggtcccga agtcgtggca ggaggaggtc gggtaataga 1440
gacagaactg ttcagagtcc caaatccaaa taaactagtt ttgttctt 1488

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&lt;210&gt; 128

&lt;211&gt; 482

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 128

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Met Ala Ala Pro Glu Lys Met Thr Phe Pro Glu Lys Pro Ser His Lys
1          5          10          15
Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg Gln
20          25          30
Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu Glu
35          40          45
Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Glu Lys Leu Leu
50          55          60
Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu Gln
65          70          75          80
Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala Ala
85          90          95
Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp Glu
100          105          110
Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Glu Gln Lys Arg Gln Glu
115          120          125
Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala Glu
130          135          140
Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro Val
145          150          155          160
Asp Phe Arg Val Met Glu Lys Asp Arg Ala Asn Cys Pro Phe Tyr Ser
165          170          175
Lys Thr Gly Ala Cys Arg Phe Gly Asp Arg Cys Ser Arg Lys His Asn
180          185          190
Phe Pro Thr Ser Ser Pro Thr Leu Leu Ile Lys Ser Met Phe Thr Thr

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195	200	205
Phe Gly Met Glu Gln Cys Arg Arg Asp Asp Tyr Asp Pro Asp Ala Ser		
210	215	220
Leu Glu Tyr Ser Glu Glu Thr Tyr Gln Gln Phe Leu Asp Phe Tyr		
225	230	235
Glu Asp Val Leu Pro Glu Phe Lys Asn Val Gly Lys Val Ile Gln Phe		240
245	250	255
Lys Val Ser Cys Asn Leu Glu Pro His Leu Arg Gly Asn Val Tyr Val		
260	265	270
Gln Tyr Gln Ser Glu Glu Glu Cys Gln Ala Ala Leu Ser Leu Phe Asn		
275	280	285
Gly Arg Trp Tyr Ala Gly Arg Gln Leu Gln Cys Glu Phe Cys Pro Val		
290	295	300
Thr Arg Trp Lys Met Ala Ile Cys Gly Leu Phe Glu Ile Gln Gln Cys		
305	310	315
Pro Arg Gly Lys His Cys Asn Phe Leu His Val Phe Arg Asn Pro Asn		
325	330	335
Asn Glu Phe Trp Glu Ala Asn Arg Asp Ile Tyr Leu Ser Pro Asp Arg		
340	345	350
Thr Gly Ser Ser Phe Gly Lys Asn Ser Glu Arg Arg Glu Arg Met Gly		
355	360	365
His His Asp Asp Tyr Tyr Ser Arg Leu Arg Gly Arg Arg Asn Pro Ser		
370	375	380
Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Ser Ser		
385	390	395
Arg His Arg Gly Lys Ser His Lys Arg Thr Ser Lys Ser Arg Glu		
405	410	415
Arg His Asn Ser Arg Ser Arg Gly Arg Asn Arg Asp Arg Ser Arg Asp		
420	425	430
Arg Ser Arg Gly Arg Gly Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg		
435	440	445
Arg Ser Arg Arg Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg		
450	455	460
Gly Arg Arg Arg Ser Gly Asn Arg Asp Arg Thr Val Gln Ser Pro Lys		
465	470	475
Ser Lys		480

&lt;210&gt; 129

&lt;211&gt; 1663

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 129

aggccctgag ccaactccgg gtgctctgct gtgagtggct gaggcccgag atccacacca	60
aggagcagat cctggagcta ctggtgctgg agcagttcct gaccatcctg cccagggagc	120
tccaggcctg ggtgcaggag cattgcccg agagcgctga agaggctgtc actctcctcg	180
aagatctgga gcgggaactg gatgagccag gacaccaggt ctcaactcct ccaaacgaac	240
agaaaccggt gtgggagaag atatcctcct caggaactgc aaaggaatcc ccgagcagca	300
tgcagccaca gcccttgagg accagtcaca aatacgagtc ttggggggccc ctgtacatcc	360
aagagtctgg tgaggagcag gagttcgctc aagatccaag aaagggtccga gattgcagat	420
tgagtaccca gcacgaggaa tcagcagatg agcagaaagg ttctgaagca gaggggctca	480
aaggggatata aatttctgtg attatcgcca ataaacctga ggccagctta gagaggcagt	540
gcgtaaacct tgaaaatgaa aaaggaacaa aacccccctct tcaagaggca ggctccaaga	600
aaggtagaga atcagttcct actaaaccta cccagggaga gagacgttat atatgtgctg	660

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aatgtggcaa agcctttagt aatagctcaa atctcaccaa acacaggaga acacacactg      720
gggagaaaacc ttacgtgtgc accaagtgtg ggaaagcttt cagccacagc tcaaacctca      780
ccctccacta cagaacacac ttggtggacc ggccctatga ctgtaagtgt ggaaaagctt      840
ttgggcagag ctcagacctt cttaaacatc agagaatgca cacagaagag gcgccatatac      900
agtgcaaaga ttgtggcaag gctttcagcg ggaaaggcag cctcattcgt cactatcgga      960
tccacactgg ggagaagcct tatcagtgtg acgaatgtgg gaagagcttc agtcagcatg     1020
cgggcctcag ctcaccaccag agactccaca ccggagagaa gccatataag tgtaaggagt     1080
gtgggaaagc cttcaaccac agctccaact tcaataaaca ccacagaatc cacaccgggg     1140
aaaagcccta ctggtgtcat cactgtggaa agaccttctg tagcaagtcc aatctttcca     1200
aacatcagcg agtccacact ggagagggag aagcaccgta actttcaagc gtcctgttg      1260
ttgtcgttgt tttaaacttt agaacttgaa aaccagaaaag aagtcttgtc attgcagcag      1320
catcgattcc ggtgatagag tttgtatcac tcaacatcag gggatgcctg aggagtgcga      1380
gctccacagc aacatggcag gcaggaggtc ctcagaaggt gtcaggaggt tccacactcg      1440
ccagttcact ggagcagagt cccttcgcca cacttagggg cccagtaagc catgccagca      1500
ttaccttttg cgtagttaaa cagacgtgta tccagtctag ttaaggaaga aacattaaga      1560
ttgtttaatt tttaacatat attcaagaat ttttaattgt aaagaattga gccacattga      1620
acacaattga atgagattca gaataaactt ataacatctt aaa                          1663

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&lt;210&gt; 130

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 130

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Ala Leu Ser Gln Leu Arg Val Leu Cys Cys Glu Trp Leu Arg Pro Glu
 1              5              10              15
Ile His Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu Gln Phe
              20              25              30
Leu Thr Ile Leu Pro Gln Glu Leu Gln Ala Trp Val Gln Glu His Cys
              35              40              45
Pro Glu Ser Ala Glu Glu Ala Val Thr Leu Leu Glu Asp Leu Glu Arg
 50              55              60
Glu Leu Asp Glu Pro Gly His Gln Val Ser Thr Pro Pro Asn Glu Gln
65              70              75              80
Lys Pro Val Trp Glu Lys Ile Ser Ser Ser Gly Thr Ala Lys Glu Ser
              85              90              95
Pro Ser Ser Met Gln Pro Gln Pro Leu Glu Thr Ser His Lys Tyr Glu
100              105              110
Ser Trp Gly Pro Leu Tyr Ile Gln Glu Ser Gly Glu Glu Gln Glu Phe
115              120              125
Ala Gln Asp Pro Arg Lys Val Arg Asp Cys Arg Leu Ser Thr Gln His
130              135              140
Glu Glu Ser Ala Asp Glu Gln Lys Gly Ser Glu Ala Glu Gly Leu Lys
145              150              155              160
Gly Asp Ile Ile Ser Val Ile Ile Ala Asn Lys Pro Glu Ala Ser Leu
              165              170              175
Glu Arg Gln Cys Val Asn Leu Glu Asn Glu Lys Gly Thr Lys Pro Pro
180              185              190
Leu Gln Glu Ala Gly Ser Lys Lys Gly Arg Glu Ser Val Pro Thr Lys
195              200              205
Pro Thr Pro Gly Glu Arg Arg Tyr Ile Cys Ala Glu Cys Gly Lys Ala
210              215              220
Phe Ser Asn Ser Ser Asn Leu Thr Lys His Arg Arg Thr His Thr Gly
225              230              235              240
Glu Lys Pro Tyr Val Cys Thr Lys Cys Gly Lys Ala Phe Ser His Ser

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245 250 255  
 Ser Asn Leu Thr Leu His Tyr Arg Thr His Leu Val Asp Arg Pro Tyr  
 260 265 270  
 Asp Cys Lys Cys Gly Lys Ala Phe Gly Gln Ser Ser Asp Leu Leu Lys  
 275 280 285  
 His Gln Arg Met His Thr Glu Glu Ala Pro Tyr Gln Cys Lys Asp Cys  
 290 295 300  
 Gly Lys Ala Phe Ser Gly Lys Gly Ser Leu Ile Arg His Tyr Arg Ile  
 305 310 315 320  
 His Thr Gly Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Ser Phe  
 325 330 335  
 Ser Gln His Ala Gly Leu Ser Ser His Gln Arg Leu His Thr Gly Glu  
 340 345 350  
 Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn His Ser Ser  
 355 360 365  
 Asn Phe Asn Lys His His Arg Ile His Thr Gly Glu Lys Pro Tyr Trp  
 370 375 380  
 Cys His His Cys Gly Lys Thr Phe Cys Ser Lys Ser Asn Leu Ser Lys  
 385 390 395 400  
 His Gln Arg Val His Thr Gly Glu Gly Glu Ala Pro  
 405 410

<210> 131  
 <211> 724  
 <212> DNA  
 <213> Homo Sapiens

<400> 131  
 ggagaatgaa aagcagaaaag tggcagagct gtattctatc cataactctg gagacaaatc 60  
 tgatattcag gacctcctgg agagtgtcag gctggacaaa gaaaaagcag agactttggc 120  
 tagtagcttg caggaagatc tggctcatc ccgaaatgat gccaatcgat tacaggatgc 180  
 cattgctaag gttagaggatg aataccgagc cttccaagaa gaagctaaga aacaaattga 240  
 agatttgaat atgacgttag aaaaattaag atcagacctg gatgaaaaag aaacagaaaag 300  
 gagtgacatg aaagaaacca tctttgaact tgaagatgaa gtagaacaac atcgtgctgt 360  
 gaaacttcat gacaacctca ttatttctga tctagagaat acagttaaaa aactccagga 420  
 ccaaaagcac gacatggaaa gagaaataaa gacactccac agaagacttc gggaagaatc 480  
 tgcggaatgg cggcagtttc aggtgatct ccagactgca gtagtcattg caaatgacat 540  
 taaatctgaa gcccaagagg agattgggtga tctaaagcgc cgggtacatg aggtcaaga 600  
 aaaaaatgag aaactcaciaa aagaattgga ggaaataagt ccgccaagcc agaagangac 660  
 gangccggtg ttccantaca tgnatgcccg tgagagagaa tttggcaggc cttaaggcag 720  
 ggaa 724

<210> 132  
 <211> 218  
 <212> PRT  
 <213> Homo Sapiens

<400> 132  
 Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile His Asn Ser  
 1 5 10 15  
 Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val Arg Leu Asp  
 20 25 30  
 Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala  
 35 40 45  
 His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile Ala Lys Val

50                      55                      60  
 Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys Gln Ile Glu  
 65                      70                      75                      80  
 Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys  
                     85                      90                      95  
 Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp  
                     100                      105                      110  
 Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile  
                     115                      120                      125  
 Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln Lys His Asp  
                     130                      135                      140  
 Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg Glu Glu Ser  
 145                      150                      155                      160  
 Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala Val Val Ile  
                     165                      170                      175  
 Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly Asp Leu Lys  
                     180                      185                      190  
 Arg Arg Val His Glu Ala Gln Glu Lys Asn Glu Lys Leu Thr Lys Glu  
                     195                      200                      205  
 Leu Glu Glu Ile Ser Pro Pro Ser Gln Lys  
                     210                      215

<210> 133  
 <211> 719  
 <212> DNA  
 <213> Homo Sapiens

<400> 133  
 gagaactaca gagctgggtg cggggccaac ggccagaaag tggcgaggag gcagtgcgc                      60  
 tgggtggaggg tttgcagaaa caaccagga gaccaaggcg gtgactgtcc atgttcacgg                      120  
 ccaggaagtc ctgtcagagg agacggtgca tttaggagcg gagcctgagt cacctaata                      180  
 getgcaggat cctgtgcaaa gctcgacccc cgagcagtc cctgaggaaa ccacacagag                      240  
 cccagatctg ggggcaccgg cagagcagcg tccacaccag gaagaggagc tccagaccct                      300  
 gcaggagagc gaggtccag tgcccagga cccagacctt cctgcagaga ggagctctgg                      360  
 agactcagag atggttgctc ttcttactgc tctgtcacag ggactggtaa cgttcaagga                      420  
 tgtggccgta tgcttttccc aggaccagtg gagtgatctg gacccaacac agaaagagtt                      480  
 ctatggagaa tatgtcttgg aagaagactg tggaattgtt gtctctctgt catttccaat                      540  
 cccagacct gatgatct cccagggttag agaggaagag cccttgggtc ccagatatcc                      600  
 aagagcctna ggagactcaa gagccagaaa tcctgagttt tacctacaca ggagatagga                      660  
 gtnaagatga aggaaaatgt ctggagccag gaagaatctg agtttggagg atataccca                      719

<210> 134  
 <211> 217  
 <212> PRT  
 <213> Homo Sapiens

<400> 134  
 Arg Thr Thr Glu Leu Gly Ala Gly Pro Thr Ala Arg Lys Trp Arg Gly  
 1                      5                      10                      15  
 Gly Ser Asp Ala Gly Gly Gly Phe Ala Glu Thr Thr Gln Glu Thr Lys  
                     20                      25                      30  
 Ala Val Thr Val His Val His Gly Gln Glu Val Leu Ser Glu Glu Thr  
                     35                      40                      45  
 Val His Leu Gly Ala Glu Pro Glu Ser Pro Asn Glu Leu Gln Asp Pro  
                     50                      55                      60

Val Gln Ser Ser Thr Pro Glu Gln Ser Pro Glu Glu Thr Thr Gln Ser  
 65 70 75 80  
 Pro Asp Leu Gly Ala Pro Ala Glu Gln Arg Pro His Gln Glu Glu Glu  
 85 90 95  
 Leu Gln Thr Leu Gln Glu Ser Glu Val Pro Val Pro Glu Asp Pro Asp  
 100 105 110  
 Leu Pro Ala Glu Arg Ser Ser Gly Asp Ser Glu Met Val Ala Leu Leu  
 115 120 125  
 Thr Ala Leu Ser Gln Gly Leu Val Thr Phe Lys Asp Val Ala Val Cys  
 130 135 140  
 Phe Ser Gln Asp Gln Trp Ser Asp Leu Asp Pro Thr Gln Lys Glu Phe  
 145 150 155 160  
 Tyr Gly Glu Tyr Val Leu Glu Glu Asp Cys Gly Ile Val Val Ser Leu  
 165 170 175  
 Ser Phe Pro Ile Pro Arg Pro Asp Glu Ile Ser Gln Val Arg Glu Glu  
 180 185 190  
 Glu Pro Leu Gly Pro Arg Tyr Pro Arg Ala Gly Asp Ser Arg Ala Arg  
 195 200 205  
 Asn Pro Glu Phe Tyr Leu His Arg Arg  
 210 215

<210> 135  
 <211> 1027  
 <212> DNA  
 <213> Homo Sapiens

<400> 135  
 gcgagggcga gggcgaggcg gtgctcatgg aggaggacct gatccagcag agcctggacg 60  
 actacgacgc cggcaggtac agcccgcggc tgctcacggc gcacgagctg ccactggacg 120  
 cgcacgtgct ggaaccggat gaggacctgc agcgctgca gctctcgcg cagcagctcc 180  
 aggtcacggg agacgccagc gagagcgccg aggacatctt cttccggcgg gccaaaggagg 240  
 gcatgggcca ggacgaggcg cagttcagcg tggagatgcc actcaccggc aaggccctacc 300  
 tgtggggcca caagtaccgg ccacgcaagc cgcgcttctt caaccgctg cacacgggct 360  
 tcgagtggaa caagtacaac cagacgcact acgactttga caaccacccg cccaagatcg 420  
 tgcagggata caagttcaac atcttctacc ccgacctcat cgacaagcgc tccacgcccg 480  
 agtacttctt ggaggcctgc gccgacaaca aggatttctg catcctgcgc ttcacgcggg 540  
 gccgcctacg aggacatcgc tttcaagatc gtcaaccgcg agtggggaata ctngcaccgc 600  
 cacggcttcc gctgccagtt tgccaacggc attttccanc tgncttttca cttcaagcgc 660  
 tnccgctatc ggcggtgacg gccctgggga acggcaggcc aggaggggcg agggccacac 720  
 ggggtgccaca gcccaggtcg gagtggccca gccggcaggc ttgtttttca gcatccgacg 780  
 ggaacatctc caacagaagc aaaacggaaa gtgcctcccg gacccccaga gggccaccca 840  
 acctcaccag tcaccagccc cagaccaccc acagcccctc ccagacaccc cgcctcatct 900  
 ggaaatagtt ccgtttgttt ctctaaaaag acttgtaggt gggaaaaaaaa atcttttggg 960  
 ctcatggaat tggcctattg gcaagatcgc atgttttttt aataaacggt gtatttttaga 1020  
 ataaaaa 1027

<210> 136  
 <211> 299  
 <212> PRT  
 <213> Homo Sapiens

<400> 136  
 Glu Gly Glu Gly Glu Ala Val Leu Met Glu Glu Asp Leu Ile Gln Gln  
 1 5 10 15  
 Ser Leu Asp Asp Tyr Asp Ala Gly Arg Tyr Ser Pro Arg Leu Leu Thr



20	25	30
Ala His Glu Leu Pro Leu Asp	Ala His Val Leu Glu Pro Asp Glu Asp	
35	40	45
Leu Gln Arg Leu Gln Leu Ser Arg	Gln Gln Leu Gln Val Thr Gly Asp	
50	55	60
Ala Ser Glu Ser Ala Glu Asp Ile Phe Phe Arg Arg Ala Lys Glu Gly		
65	70	75
Met Gly Gln Asp Glu Ala Gln Phe Ser Val Glu Met Pro Leu Thr Gly		
85	90	95
Lys Ala Tyr Leu Trp Ala Asp Lys Tyr Arg Pro Arg Lys Pro Arg Phe		
100	105	110
Phe Asn Arg Val His Thr Gly Phe Glu Trp Asn Lys Tyr Asn Gln Thr		
115	120	125
His Tyr Asp Phe Asp Asn Pro Pro Pro Lys Ile Val Gln Gly Tyr Lys		
130	135	140
Phe Asn Ile Phe Tyr Pro Asp Leu Ile Asp Lys Arg Ser Thr Pro Glu		
145	150	155
Tyr Phe Leu Glu Ala Cys Ala Asp Asn Lys Asp Phe Ala Ile Leu Arg		
165	170	175
Phe Thr Arg Gly Arg Leu Arg Gly His Arg Phe Gln Asp Arg Gln Pro		
180	185	190
Arg Val Gly Ile Leu Ala Pro Pro Arg Leu Pro Leu Pro Val Cys Gln		
195	200	205
Arg His Phe Pro Leu Ser Leu Gln Ala Leu Pro Leu Ser Ala Val Thr		
210	215	220
Ala Leu Gly Asn Gly Arg Pro Gly Gly Pro Arg Ala Thr Arg Val Pro		
225	230	235
Gln Pro Arg Ser Glu Trp Pro Ser Arg Gln Ala Cys Phe Ser Ala Ser		
245	250	255
Asp Gly Asn Ile Ser Asn Arg Ser Lys Thr Glu Ser Ala Ser Arg Thr		
260	265	270
Pro Arg Gly Pro Pro Asn Leu Thr Ser His Gln Pro Gln Thr Thr His		
275	280	285
Ser Pro Ser Gln Thr Pro Arg Leu Ile Trp Lys		
290	295	

&lt;210&gt; 137

&lt;211&gt; 766

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 137

caaagggttta	cacagtaaac	aatgtgaatg	tgatcaccaa	aatacgcaca	gaacatctga	60
ccgaggagga	aaaaaagaga	tataaagaca	ggaacccgct	ggaatctttg	ctgggaactg	120
tggaacacca	atttggtgca	caaggggacc	tcaccacgga	atgtgctact	gcaaacaacc	180
ccacagccat	cacgcctgat	gagtacttca	atgaagagtt	tgatctgaaa	gacagggaca	240
ttggaaggcc	gaaagagctg	acgattagaa	cacagaagtt	taaagcaatg	ttgtggatgt	300
gtgaagagtt	ccccctctct	ctggtggagc	aggtcattcc	catcattgac	ctaattggctc	360
gaacgagtgc	tcattttgca	agactgagag	atttcatcaa	attggaattc	ccacctggat	420
ttcctgtcaa	aatagcttcc	cacatcacaa	actttgaggt	tgatcaatct	gtgtttgaaa	480
ttcccgaatc	ttactatggt	caagacaatg	gcagaaatgt	gcatttgcaa	gatgaagatt	540
acgagataat	gcagtttgcc	atccagcaaa	gtctgctgga	gtccagcagg	agccaggaac	600
tttcaggacc	agcttcgaat	ggaggggatca	gccagacaaa	cacctatgac	gcccagtatg	660
agagggccat	ncaggagagc	cttctaccag	cacagagagc	ctgtgcccc	agcgcccctg	720
agcgagacna	gccgttttga	taatggactt	gcagagagag	catgga		766

<210> 138  
 <211> 243  
 <212> PRT  
 <213> Homo Sapiens

<400> 138  
 Lys Val Tyr Thr Val Asn Asn Val Asn Val Ile Thr Lys Ile Arg Thr  
 1 5 10 15  
 Glu His Leu Thr Glu Glu Glu Lys Lys Arg Tyr Lys Asp Arg Asn Pro  
 20 25 30  
 Leu Glu Ser Leu Leu Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly  
 35 40 45  
 Asp Leu Thr Thr Glu Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr  
 50 55 60  
 Pro Asp Glu Tyr Phe Asn Glu Glu Phe Asp Leu Lys Asp Arg Asp Ile  
 65 70 75 80  
 Gly Arg Pro Lys Glu Leu Thr Ile Arg Thr Gln Lys Phe Lys Ala Met  
 85 90 95  
 Leu Trp Met Cys Glu Glu Phe Pro Leu Ser Leu Val Glu Gln Val Ile  
 100 105 110  
 Pro Ile Ile Asp Leu Met Ala Arg Thr Ser Ala His Phe Ala Arg Leu  
 115 120 125  
 Arg Asp Phe Ile Lys Leu Glu Phe Pro Pro Gly Phe Pro Val Lys Ile  
 130 135 140  
 Ala Ser His Ile Thr Asn Phe Glu Val Asp Gln Ser Val Phe Glu Ile  
 145 150 155 160  
 Pro Glu Ser Tyr Tyr Val Gln Asp Asn Gly Arg Asn Val His Leu Gln  
 165 170 175  
 Asp Glu Asp Tyr Glu Ile Met Gln Phe Ala Ile Gln Gln Ser Leu Leu  
 180 185 190  
 Glu Ser Ser Arg Ser Gln Glu Leu Ser Gly Pro Ala Ser Asn Gly Gly  
 195 200 205  
 Ile Ser Gln Thr Asn Thr Tyr Asp Ala Gln Tyr Glu Arg Ala Gln Glu  
 210 215 220  
 Ser Leu Leu Pro Ala Gln Lys Ala Cys Ala Pro Ser Ala Pro Glu Arg  
 225 230 235 240  
 Asp Pro Phe

<210> 139  
 <211> 3060  
 <212> DNA  
 <213> Homo Sapiens

<400> 139  
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 gcggcgggcg cagcgggcgg gcgggggctg tggggcggtg cggaagcgag aggcgaggag 120  
 cgcgcgggcc gtggccagag tctggcgggc gcctggcgga gcggagagca gcgcccgcgc 180  
 ctgcgctgct ggaggagccc cgcacacaat agcggcgcgc gcagcccgcg cccttcccc 240  
 cggcgcgccc cgccccgcgc gccgagcgcc ccgctccgcc tcacctgcca ccagggagtg 300  
 ggcgggcatt gttcgccgcc gccgcgcgc cgcggggcca tgggggcccgc ccggcgcccgc 360  
 gggccgggccc tggcgaggcc gccgcgcgc cgtgagagcg ggccccgcgc gcagcccggc 420  
 ggcgaggtta aggcgggccc cgccatgggt gacccgggtg gcttcggcgga ggcggtggaag 480  
 gcgcagttcc cggactcaga gccccgcgc atggagcttc gcttcagtgga cgacatcgag 540  
 caggagctgg agcgtcgcaa ggccctcatt cggcgccctg agcaggaggt gaaccaggag 600

cgtttccgca	tgatctacct	gcagacgttg	ctggccaagg	aaaagaagag	ctatgaccgg	660
cagcgaatggg	gctttccggcg	cgcgccgcag	gcccccgacg	gcgcctccga	gccccgagcg	720
tccgcgtcgc	gccccgcagcc	agcgccccgc	gacggagccg	acccgccgcc	cgccgaggag	780
cccgaaggccc	ggccccgacgg	cgaggggtct	ccgggtaagg	ccaggccccg	gaccgccccg	840
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gcgctcaggt	ccaacttcga	gcggatccgc	aaggggccatg	gccagccccg	ggcgagacgc	960
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aaaaagtccc	agcacggcgc	gggctcgagc	gtgggggatg	catccaggcc	cccttaccgg	1140
ggacgctcct	cggagagcag	ctgcggcgct	gacggcgact	acgaggacgc	cgagttgaac	1200
ccccgcttcc	tgaaggacaa	cctgatcgac	gccaatggcg	gtagcaggcc	cccttggccg	1260
cccctggagt	accagcccta	ccagagcacc	tacgtcgggg	gcatgatgga	aggggagggc	1320
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gtgtccccaa	gccccaccac	ctaccgcag	ttccgggaca	aaagccgctc	tcctctcgag	1560
aactcgcaac	agtcccttga	cagcagcagt	ccccccacgc	cgcagtgcc	taagcggcac	1620
cggcactgcc	cggttgtcgt	gtccgagggc	accatcgtgg	gcgtccgcaa	gaccgggcag	1680
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gaaaaggggt	tggagatgag	aaaatgggtc	ctgtcgggaa	tcctggctag	cgaggagact	1980
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ctctacgaga	tccacaagga	gttctatgat	gggctcttcc	cccgcgtgca	gcagtggagc	2160
caccagcagc	gggtgggcga	cctcttccag	aagctggcca	gccagctggg	tgtgtaccgg	2220
gccttcgtgg	acaactacgg	agttgccatg	gaaatggctg	agaagtgtct	tcaggccaat	2280
gctcagtttg	cagaaatctc	cgagaacctg	agagccagaa	gcaacaaaga	tgccaaggat	2340
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aggctgaaga	agaagctgtc	ggagcaggag	tcactgctgc	tgcttatgtc	tcccagcatg	2940
gccttcaggg	tgcacagccg	caacggcaag	agttacacgt	tcctgatctc	ctctgactat	3000
gagcgtgcag	agtggaggga	gaacatccgg	gagcagcaga	agaagtgttt	cagaagcttc	3060

&lt;210&gt; 140

&lt;211&gt; 872

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 140

Met	Val	Asp	Pro	Val	Gly	Phe	Ala	Glu	Ala	Trp	Lys	Ala	Gln	Phe	Pro
1				5					10					15	
Asp	Ser	Glu	Pro	Pro	Arg	Met	Glu	Leu	Arg	Ser	Val	Gly	Asp	Ile	Glu
			20					25					30		
Gln	Glu	Leu	Glu	Arg	Cys	Lys	Ala	Ser	Ile	Arg	Arg	Leu	Glu	Gln	Glu
		35					40					45			
Val	Asn	Gln	Glu	Arg	Phe	Arg	Met	Ile	Tyr	Leu	Gln	Thr	Leu	Leu	Ala

50 55 60  
 Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala  
 65 70 75 80  
 Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg  
 85 90 95  
 Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu  
 100 105 110  
 Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro  
 115 120 125  
 Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp  
 130 135 140  
 Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg  
 145 150 155 160  
 Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe  
 165 170 175  
 Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn  
 180 185 190  
 Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met  
 195 200 205  
 Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly  
 210 215 220  
 Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys  
 225 230 235 240  
 Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu  
 245 250 255  
 Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro  
 260 265 270  
 Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met  
 275 280 285  
 Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu  
 290 295 300  
 Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser  
 305 310 315 320  
 Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu  
 325 330 335  
 Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg  
 340 345 350  
 Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg  
 355 360 365  
 Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Pro Pro  
 370 375 380  
 Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser  
 385 390 395 400  
 Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn  
 405 410 415  
 Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr  
 420 425 430  
 Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg  
 435 440 445  
 His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro  
 450 455 460  
 His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly  
 465 470 475 480  
 Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu  
 485 490 495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr  
 500 505 510  
 Tyr Leu Ser His Leu Glu Ala Leu Leu Pro Met Lys Pro Leu Lys  
 515 520 525  
 Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu  
 530 535 540  
 Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe  
 545 550 555 560  
 Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg  
 565 570 575  
 Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg  
 580 585 590  
 Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys  
 595 600 605  
 Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala  
 610 615 620  
 Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu  
 625 630 635 640  
 Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val  
 645 650 655  
 Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro  
 660 665 670  
 Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile  
 675 680 685  
 Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly  
 690 695 700  
 Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu  
 705 710 715 720  
 Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu  
 725 730 735  
 Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp  
 740 745 750  
 Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp  
 755 760 765  
 Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu  
 770 775 780  
 Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg  
 785 790 795 800  
 Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys  
 805 810 815  
 Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Met Ser Pro Ser Met  
 820 825 830  
 Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile  
 835 840 845  
 Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln  
 850 855 860  
 Gln Lys Lys Cys Phe Arg Ser Phe  
 865 870

&lt;210&gt; 141

&lt;211&gt; 691

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 141

```

gacccctcac actcacctag ccaccatgga catcgccatc caccacccct ggatccgcgcg      60
ccccctcttt cctttccact ccccagccg cctctttgac cagttcttcg gagagcacct      120
gttgaggtct gatcttttcc cgacgtctac ttccctgagt ccttctacc ttcggccacc      180
ctccttcttg cgggcaccca gctggtttga cactggactc tcagagatgc gcctggagaa      240
ggacagggttc tctgtcaacc tggatgtgaa gcacttctcc ccagaggaaac tcaaagttaa      300
ggtgttgga gatgtgattg aggtgcatgg aaaacatgaa gagcgccagg atgaacatgg      360
tttcatctcc agggagttcc acaggaaata ccgatccca gctgatgtag accctctcac      420
cattacttca tccctgtcat ctgatgggt cctcactgtg aatggacca gaaacaggt      480
ctctggccct gagcgacca ttcccatcac ccgtgaagag aagcctgctg tcaccgcagc      540
ccccaagaaa tagatgcct ttcttgaatt gcatttttta aaacaagaaa gtttccccac      600
cagtgaatga aagtcttctg actagtgtg aagcttatta atgctaaggg caggcccaaa      660
ttatcaagct aataaaatat cattcagcaa c      691

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&lt;210&gt; 142

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 142

```

Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
 1          5          10          15
Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
 20          25          30
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
 35          40          45
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
 50          55          60
Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
 65          70          75          80
Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
 85          90          95
Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
100          105          110
Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
115          120          125
Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
130          135          140
Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145          150          155          160
Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
165          170          175

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&lt;210&gt; 143

&lt;211&gt; 1300

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 143

```

atctgctggg aatttcttgg gttgacagct cttggatccc tattttgaac agtggtagtg      60
tcctggatta cttttcagaa agaagtaatc ctttttatga cagaacatgt aataatgaag      120
tggtcaaaat gcagaggcta acattagaac acttgaatca gatggttgga atcgagtaca      180
tccttttgca tgctcaagag ccattcttt tcatcattcg gaagcaacag cggcagtcct      240
ctgcccaggt tatccacta gctgattact atatcattgc tggagtgatc tatcaggcac      300
cagacttggg atcagttata aactctagag tgcttactgc agtgcattgg attcagtcag      360
cttttgatga agctatgtca tactgtcgat atcatccttc caaaggggtat tgggtggcact      420

```

```

tcaaagatca tgaagagcaa gataaagtca gacctaaagc caaaaggaaa gaagaaccaa 480
gctctatddd tcagagacaa cgtgtggatg ctttactddd agacctcaga caaaaatttc 540
cacccaaatt tgtgcagcta aagcctggag aaaagcctgt tcaagtggat caaacaaga 600
aagaggcaga acctatacca gaaactgtaa aacctgagga gaaggagacc ccnnnagaat 660
gtacaaccag accgggagtg ctaaaggccc ccctgaaaaa cggatgagac ttcagtgagt 720
actggacaaa agagaagcct ggaagactcc tcatgctagt tatcatacct cagtactgtg 780
gctcttgagc tttgaagtac tttattgtaa ccttcttatt tgtatggaat gcgcttattt 840
tttgaaagga tattaggccg gatgtggtgg ctcacgcctg taatcccagc actttgggag 900
gccatggcgg gtggatcact tgaggtcaga agttcaagac cagcctgacc aatatggtga 960
aaccctgtct ctactaaaaa taaaaaaatt agccgggcgt ggtggcgggc gccctagtc 1020
ccagctactc gggaggctga gacaggagac ttgcttgaac ccgggaggtg gaggttgccc 1080
tgagctgatt atcatgctgt tgcactccag cttgggcgac agagcgagac tttgtctcaa 1140
aaaagaagaa aagatattac tcccatcatg atttcttgtg aatatttgtt atatgtcttc 1200
tgtaaccttt cctctcccgg acttgagcaa cctacacact cacatgttta ctggtagata 1260
tgtttaaaag caaaataaag gtatttgtat atattgaaaa 1300

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&lt;210&gt; 144

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 144

```

Leu Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu Asn
1          5          10          15
Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr
20        25        30
Asp Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr Leu
35        40        45
Glu His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala
50        55        60
Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro
65        70        75        80
Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile
85        90        95
Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr
100       105       110
Ala Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys
115       120       125
Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu
130       135       140
Glu Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser
145       150       155       160
Ser Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg
165       170       175
Gln Lys Phe Pro Pro Lys Phe Val Gln Leu Lys Pro Gly Glu Lys Pro
180       185       190
Val Gln Val Asp Gln Thr Lys Lys Glu Ala Glu Pro Ile Pro Glu Thr
195       200       205
Val Lys Pro Glu Glu Lys Glu Thr Pro Glu Cys Thr Thr Arg Pro Gly
210       215       220
Val Leu Lys Ala Pro Leu Lys Asn Gly
225       230

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&lt;210&gt; 145

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 145

```

ccccccctttt tttttaaact aaaatggagg ctggtttctt gccttaagga gccattgcc      60
tttcccgctg aagtcctagat gttgacatgt aataaagcgg gcagcaggat ggtgggtggat      120
gcgccaact ccaatgggcc tttccagccc gtggtccttc tccatattcg agatgttctt      180
cctgctgac aagagaagct ttttatccag aagttacgtc agtggtgcgt cctctttgac      240
tttgtttctg atccactaag tgacctaaag tggaaggaag taaaacgagc tgctttaagt      300
gaaatggtag aatatatcac ccataatcgg aatgtgatca cagagcctat ttaccagaa      360
gtagtccata tgtttgcagt taacatgttt cgaacattac caccttcctc caatcctacg      420
ggagcggaaat ttgaccggga ggaagatgaa ccaacgtag aagcagcctg gcctcatcta      480
cagcttgttt atgaattttt cttagatttt ttagagtctc cagatttcca acctaatata      540
gcgaagaaat atattgatca gaagtttgta ttgcagcttt tagagctctt tgacagtga      600
gatcctcggg agagagattt tcttaaaacc acccttcaca gaatctatgg gaaattccta      660
ggcttgagag cttacatcag aaaacagata aataatatat tttatagggt tatttatgaa      720
acagagcatc ataatggcat agcagagtta ctggaaatat tgggaagtat aattaatgga      780
tttgccctac cactaaaaga agagcacaag attttcttat tgaagggtgt actacctttg      840
cacaaagtga aatctctgag tgtctaccat cccagctgg catactgtgt agtgcagttt      900
ttagaaaagg acagcaccct cacggaacca gtgggtgatgg cacttctcaa atactggcca      960
aagactcaca gtccaaaaga agtaatgttc ttaaacgaat tagaagagat tttagatgtc     1020
attgaaccat cagaatttgt gaagatcatg gaacccctct tccggcagtt ggccaaatgt     1080
gtctccagcc cacacttcca ggtggcagag cgagctctct attactggaa taatgaatac     1140
atcatgagtt taatcagtga caacgcagcg aagattctgc ccatcatgtt tcttctcttg     1200
taccgcaact caaagaccca ttggaacaag acaatacatg gcttgatata caacgccttg     1260
aagctcttca tggagatgaa ccaaaagcta tttgatgact gtacacaaca gttcaaagca     1320
gagaaactaa aagagaagct aaaaatgaaa gaacgggaag aagcatgggt taaaatagaa     1380
aatctagcca aagccaatcc ccaggtacta aaaaagagaa taacatgaaa aggcccaggg     1440
ttacttgaat gtttttataa gataggaata tatgtcttca ccatgggggg ggtctcgatt     1500
tcactaacgt tgtatatgaa aatgtctg                                     1528

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&lt;210&gt; 146

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 146

```

Met Leu Thr Cys Asn Lys Ala Gly Ser Arg Met Val Val Asp Ala Ala
1           5           10           15
Asn Ser Asn Gly Pro Phe Gln Pro Val Val Leu Leu His Ile Arg Asp
20           25           30
Val Pro Pro Ala Asp Gln Glu Lys Leu Phe Ile Gln Lys Leu Arg Gln
35           40           45
Cys Cys Val Leu Phe Asp Phe Val Ser Asp Pro Leu Ser Asp Leu Lys
50           55           60
Trp Lys Glu Val Lys Arg Ala Ala Leu Ser Glu Met Val Glu Tyr Ile
65           70           75           80
Thr His Asn Arg Asn Val Ile Thr Glu Pro Ile Tyr Pro Glu Val Val
85           90           95
His Met Phe Ala Val Asn Met Phe Arg Thr Leu Pro Pro Ser Ser Asn
100          105          110
Pro Thr Gly Ala Glu Phe Asp Pro Glu Glu Asp Glu Pro Thr Leu Glu
115          120          125
Ala Ala Trp Pro His Leu Gln Leu Val Tyr Glu Phe Leu Arg Phe
130          135          140

```



Leu Glu Ser Pro Asp Phe Gln Pro Asn Ile Ala Lys Lys Tyr Ile Asp  
 145 150 155 160  
 Gln Lys Phe Val Leu Gln Leu Leu Glu Leu Phe Asp Ser Glu Asp Pro  
 165 170 175  
 Arg Glu Arg Asp Phe Leu Lys Thr Thr Leu His Arg Ile Tyr Gly Lys  
 180 185 190  
 Phe Leu Gly Leu Arg Ala Tyr Ile Arg Lys Gln Ile Asn Asn Ile Phe  
 195 200 205  
 Tyr Arg Phe Ile Tyr Glu Thr Glu His His Asn Gly Ile Ala Glu Leu  
 210 215 220  
 Leu Glu Ile Leu Gly Ser Ile Ile Asn Gly Phe Ala Leu Pro Leu Lys  
 225 230 235 240  
 Glu Glu His Lys Ile Phe Leu Leu Lys Val Leu Leu Pro Leu His Lys  
 245 250 255  
 Val Lys Ser Leu Ser Val Tyr His Pro Gln Leu Ala Tyr Cys Val Val  
 260 265 270  
 Gln Phe Leu Glu Lys Asp Ser Thr Leu Thr Glu Pro Val Val Met Ala  
 275 280 285  
 Leu Leu Lys Tyr Trp Pro Lys Thr His Ser Pro Lys Glu Val Met Phe  
 290 295 300  
 Leu Asn Glu Leu Glu Glu Ile Leu Asp Val Ile Glu Pro Ser Glu Phe  
 305 310 315 320  
 Val Lys Ile Met Glu Pro Leu Phe Arg Gln Leu Ala Lys Cys Val Ser  
 325 330 335  
 Ser Pro His Phe Gln Val Ala Glu Arg Ala Leu Tyr Tyr Trp Asn Asn  
 340 345 350  
 Glu Tyr Ile Met Ser Leu Ile Ser Asp Asn Ala Ala Lys Ile Leu Pro  
 355 360 365  
 Ile Met Phe Pro Ser Leu Tyr Arg Asn Ser Lys Thr His Trp Asn Lys  
 370 375 380  
 Thr Ile His Gly Leu Ile Tyr Asn Ala Leu Lys Leu Phe Met Glu Met  
 385 390 395 400  
 Asn Gln Lys Leu Phe Asp Asp Cys Thr Gln Gln Phe Lys Ala Glu Lys  
 405 410 415  
 Leu Lys Glu Lys Leu Lys Met Lys Glu Arg Glu Glu Ala Trp Val Lys  
 420 425 430  
 Ile Glu Asn Leu Ala Lys Ala Asn Pro Gln Val Leu Lys Lys Arg Ile  
 435 440 445  
 Thr

<210> 147  
 <211> 1580  
 <212> DNA  
 <213> Homo Sapiens

<400> 147  
 atccccctcgc gttttcctca gtctccacgt acgtccctca aagcgcgtcc taaaaccgcg 60  
 ataaccggag cgctcccat ggaccacag gagggcttgc ccgcggagga gccgcctgcg 120  
 catgctccat cgcctgggaa atttggtgag cggcctccac ctaaacgact tactagggaa 180  
 gctatgcgaa attatttaaa agagcgagg gatcaaacag tacttattct tcatgcaaaa 240  
 gttgcacaga agtcatatgg aaatgaaaaa aggtttttt gccacctcc ttgtgtatat 300  
 cttatgggca gcggatggaa gaaaaaaaaa gaacaaatgg aacgcgatgg ttgttctgaa 360  
 caagagtctc aaccgtgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420  
 ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtatatatc tgactcagac 480

```

aagcgaaagc acttcatttt ttctgtaaag atgttctatg gcaacagtga tgacattggt      540
gtgttcctca gcaagcggat aaaagtcac tcacaaacctt ccaaaaagaa gcagtcattg      600
aaaaatgctg acttatgcat tgccctcagga acaaagggtg ctctgtttta tgcactacga      660
tcccagacag ttagtaccag atacttgcac gtagaaggag gtaattttca tgcagttca      720
cagcagtggt gagccttttt tattcatctc ttggatgatg atgaatcaga aggagaagaa      780
ttcacagtcc gagatgtcta catccattat ggacaaacat gcaaacttgt gtgctcagtt      840
actggcatgg cactcccaag attgataatt atgaaagtgt ataagcatac cgcattattg      900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat ttaccttaa ggatacagaa      960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca     1020
aaagaaccaa ataaagagat gataaatgat ggcgcttctt ggacaatcat tagcacagat     1080
aaggcagagt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg     1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca     1200
ggacagaatt tcaactccaa tttacgagtg tggtttgggg atgtagaagc tgaactatg     1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt     1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tggtcgaaa tgatggaatc     1380
atattattcca ccagccttac ctttacctac acaccagaac cagggccacg gccacattgc     1440
agtgtagcag gagcaatcct tccagccaat tcaagccagg tgccccctaa cgaatcaaac     1500
acaaacagcg agggaagtta cacaaacgcc agcacaaatt caaccagtgt cacatcatct     1560
acagccacag tggatccta                                     1580

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&lt;210&gt; 148

&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 148

```

Met Asp His Thr Glu Gly Leu Pro Ala Glu Glu Pro Pro Ala His Ala
 1              5              10              15
Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr
      20              25              30
Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val
      35              40              45
Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys
      50              55              60
Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp
      65              70              75              80
Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu
      85              90              95
Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met
      100              105              110
Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu
      115              120              125
Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Ile Phe Ser Val Lys
      130              135              140
Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg
      145              150              155              160
Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn
      165              170              175
Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg
      180              185              190
Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly
      195              200              205
Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His Leu
      210              215              220
Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Val

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225                      230                      235                      240  
 Tyr Ile His Tyr Gly Gln Thr Cys Lys Leu Val Cys Ser Val Thr Gly  
                                  245                      250                      255  
 Met Ala Leu Pro Arg Leu Ile Ile Met Lys Val Asp Lys His Thr Ala  
                                  260                      265                      270  
 Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys Cys Ala Phe  
                                  275                      280                      285  
 Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser Gln Glu Arg  
                                  290                      295                      300  
 Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro Asn Lys Glu  
 305                                   310                      315                      320  
 Met Ile Asn Asp Gly Ala Ser Trp Thr Ile Ile Ser Thr Asp Lys Ala  
                                  325                      330                      335  
 Glu Tyr Thr Phe Tyr Glu Gly Met Gly Pro Val Leu Ala Pro Val Thr  
                                  340                      345                      350  
 Pro Val Pro Val Val Glu Ser Leu Gln Leu Asn Gly Gly Gly Asp Val  
                                  355                      360                      365  
 Ala Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu Arg Val  
                                  370                      375                      380  
 Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser  
 385                                   390                      395                      400  
 Met Leu Cys Val Val Pro Asp Ile Ser Ala Phe Arg Glu Gly Trp Arg  
                                  405                      410                      415  
 Trp Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp  
                                  420                      425                      430  
 Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro  
                                  435                      440                      445  
 Gly Pro Arg Pro His Cys Ser Val Ala Gly Ala Ile Leu Pro Ala Asn  
                                  450                      455                      460  
 Ser Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser  
 465                                   470                      475                      480  
 Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala  
                                  485                      490                      495  
 Thr Val Val Ser  
                                  500

&lt;210&gt; 149

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 149

caagatatcg aattccaaat ttgagggcct cccggctctg gcgccggagg gagagctcag 60  
 gccgccatgc ggcacaggac ccacgagctg agacagggg atgacagctc ggacgaagag 120  
 gacaaggagc ggggtcgcgt ggtggtgcac ccgggcacgg cacggctggg gagcccgac 180  
 gaggagtctc tccacaaggt ccggacaatt cgtcagacta ttgtcaaact gggaataaaa 240  
 gtccaggagt tggagaaaca gcaggtcacc atcctggcca cgcccccttc cgaggagagc 300  
 atgaagcagg agctgcagaa cctgcgcgat gagatcaaac agctggggag ggagatccgc 360  
 ctgcagctga aggccataga gcccagaag gaggaagctg atgagaacta taactccgtc 420  
 aacacaagaa tgagaaaaac ccagcatggg gtccgtgccc agcaattcgt ggagctcatc 480  
 aacaagtgca attcaatgca gtccgaatac cgggagaaga acgtggagcg gattcggagg 540  
 cagctgaaga tcaccaatgc tggcatgggt tctgatgagg agttggatca gatgctggac 600  
 agtgggcaaa gcgaggtggt tgtgtccaat atccttaagg acacgcaggt gactcgacag 660  
 gccttaaatg agatctcggc ccggcacagt gagatccagc agcttgaacg cagtattcgt 720  
 gagctgcacg acatattcac ttttctggct accgaagtgg agatgcaggg ggagatgac 780

```

aatcggattg agaagaacat cctgagctca gcggactacg tggaacgtgg gcaggagcac      840
gtcaagacgg ccctggagaa ccagaagaag gtgaggaaga agaaagtctt gattgccatc      900
tgtgtgtcca tcaccgtcgt cctcctagca gtcatcattg gcgtcacagt gggtggataa      960
tgtcgcacat tggtggcact aggagcacca ggaacccagg gcctggcctt ctctcccagc     1020
agcctggggg gcaggcagag cctccagtcg gaccccttcc tcacacactg gcccctatgc     1080
agaagggcag acagttcttc tgggggttggc agctgctcat tcatgatggc ctctccttcc     1140
aggcctcaat gcctggggga ggcctgcact gtcttgattg gccgggacac acggttttgt     1200
aaaaaattaa aaaacaaaaa aagagcatag aaaaaaaaaa aaccgagt                     1248

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&lt;210&gt; 150

&lt;211&gt; 297

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 150

```

Met Arg Asp Arg Thr His Glu Leu Arg Gln Gly Asp Asp Ser Ser Asp
  1          5          10          15
Glu Glu Asp Lys Glu Arg Val Ala Leu Val Val His Pro Gly Thr Ala
  20          25          30
Arg Leu Gly Ser Pro Asp Glu Glu Phe Phe His Lys Val Arg Thr Ile
  35          40          45
Arg Gln Thr Ile Val Lys Leu Gly Asn Lys Val Gln Glu Leu Glu Lys
  50          55          60
Gln Gln Val Thr Ile Leu Ala Thr Pro Leu Pro Glu Glu Ser Met Lys
  65          70          75          80
Gln Glu Leu Gln Asn Leu Arg Asp Glu Ile Lys Gln Leu Gly Arg Glu
  85          90          95
Ile Arg Leu Gln Leu Lys Ala Ile Glu Pro Gln Lys Glu Glu Ala Asp
 100          105          110
Glu Asn Tyr Asn Ser Val Asn Thr Arg Met Arg Lys Thr Gln His Gly
 115          120          125
Val Leu Ser Gln Gln Phe Val Glu Leu Ile Asn Lys Cys Asn Ser Met
 130          135          140
Gln Ser Glu Tyr Arg Glu Lys Asn Val Glu Arg Ile Arg Arg Gln Leu
 145          150          155          160
Lys Ile Thr Asn Ala Gly Met Val Ser Asp Glu Glu Leu Asp Gln Met
 165          170          175
Leu Asp Ser Gly Gln Ser Glu Val Phe Val Ser Asn Ile Leu Lys Asp
 180          185          190
Thr Gln Val Thr Arg Gln Ala Leu Asn Glu Ile Ser Ala Arg His Ser
 195          200          205
Glu Ile Gln Gln Leu Glu Arg Ser Ile Arg Glu Leu His Asp Ile Phe
 210          215          220
Thr Phe Leu Ala Thr Glu Val Glu Met Gln Gly Glu Met Ile Asn Arg
 225          230          235          240
Ile Glu Lys Asn Ile Leu Ser Ser Ala Asp Tyr Val Glu Arg Gly Gln
 245          250          255
Glu His Val Lys Thr Ala Leu Glu Asn Gln Lys Lys Val Arg Lys Lys
 260          265          270
Lys Val Leu Ile Ala Ile Cys Val Ser Ile Thr Val Val Leu Leu Ala
 275          280          285
Val Ile Ile Gly Val Thr Val Val Gly
 290          295

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&lt;210&gt; 151

&lt;211&gt; 1953

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 151

```

acgcctgcc  ggagcaagcc  gaagagccag  ccggccggcg  cactccgact  ccgagcagtc      60
tctgtccttc  gacccgagcc  ccgcgccctt  tccgggaccc  ctgccccgcg  ggcagcgctg     120
ccaacctgcc  ggccatggag  accccgtccc  agcggcgcg  caccgcagc  ggggcgcagg     180
ccagctccac  tccgctgtcg  cccaccgcga  tcaccgggt  gcaggagaag  gaggacctgc     240
aggagctcaa  tgatcgcttg  gcggtctaca  tcgaccgtgt  gcgctcgctg  gaaacggaga     300
acgcagggct  gcgccttcgc  atcaccgagt  ctgaagaggt  ggtcagccgc  gaggtgtccg     360
gcatcaaggc  cgcctacgag  gccgagctcg  gggatgccc  caagaccctt  gactcagtag     420
ccaaggagcg  cgcccgctg  cagctggagc  tgagcaaagt  gcgtgaggag  tttaaggagc     480
tgaaagcgcg  caataccaag  aaggaggggt  acctgatagc  tgctcaggct  cggctgaagg     540
acctggaggg  tctgctgaac  tccaaggagg  ccgcactgag  cactgctctc  agtgagaagc     600
gcacgctgga  gggcgagctg  catgatctgc  ggggccaggt  ggccaagctt  gaggcagccc     660
taggtgaggg  caagaagcaa  cttcaggatg  agatgctg  gcgggtggat  gctgagaaca     720
ggctgcagac  catgaaggag  gaactggact  tccagaagaa  catctacagt  gaggagctgc     780
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1953

&lt;210&gt; 152

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 152

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Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
 1             5             10             15
Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
          20             25             30
Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
          35             40             45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
          50             55             60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65             70             75             80

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Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala  
                     85                    90                    95  
 Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu  
                     100                    105                    110  
 Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile  
                     115                    120                    125  
 Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys  
                     130                    135                    140  
 Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly  
 145                    150                    155                    160  
 Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu  
                     165                    170                    175  
 Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp  
                     180                    185                    190  
 Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys  
                     195                    200                    205  
 Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr  
                     210                    215                    220  
 Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg  
 225                    230                    235                    240  
 Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val  
                     245                    250                    255  
 Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp  
                     260                    265                    270  
 Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala  
                     275                    280                    285  
 His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala  
                     290                    295                    300  
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 305                    310                    315                    320  
 Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg  
                     325                    330                    335  
 Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met  
                     340                    345                    350  
 Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala  
                     355                    360                    365  
 Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu  
                     370                    375                    380  
 Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly  
 385                    390                    395                    400  
 Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr  
                     405                    410                    415  
 Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln  
                     420                    425                    430  
 His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu  
                     435                    440                    445  
 Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met  
                     450                    455                    460  
 Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr  
 465                    470                    475                    480  
 Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr  
                     485                    490                    495  
 Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu  
                     500                    505                    510  
 Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

515                      520                      525  
 Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val  
 530                      535                      540  
 Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp  
 545                      550                      555                      560  
 Leu Leu His His His His Val Ser Gly Ser Arg Arg  
                          565                      570

<210> 153  
 <211> 1610  
 <212> DNA  
 <213> Homo Sapiens

<400> 153  
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 cgggcctttg tgaaaatgtg taagcaggat ccgagcggtt tgtacaccga ggaaatgcgc 180  
 ttcttgaggg agtgggtgga gagcataggt ggtaaagtac cacctgctac tcagaaagct 240  
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 atgatggatc aggcaaatga taaaaaagt gctgctattg aagccctaaa tgatggtgaa 480  
 ctccagaaag ccattgactt attcacagat gccatcaagc tgaatcctcg cttggccatt 540  
 ttgtatgcc aaggggccag tgtcttcgtc aaattacaga agccaaatgc tgccatccga 600  
 gactgtgaca gagccattga aataaatcct gattcagctc agccttacia gtggcggggg 660  
 aaagcacaca gacttctagg ccactgggaa gaagcagccc atgatcttgc ccttgctgt 720  
 aaattggatt atgatgaaga tgctagtga atgctgaaag aagttcaacc tagggcacag 780  
 aaaattgcag aacatcggag aaagtatgag cgaaaacgtg aagagcgaga gatcaaagaa 840  
 agaatagaac gagttaagaa ggctcgagaa gagcatgaga gagccagag ggaggaagaa 900  
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 ccattagggt attcattcag ataattgttt cctactagga attacaaact ttaaacactt 1440  
 tttaaatctt caaaatatatt aaaacaaatt taaagggcct gtttaattctt atatttttct 1500  
 ttactaatca ttttggattt ttttctttga attattggca gggaatatac ttatgtatgg 1560  
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<210> 154  
 <211> 369  
 <212> PRT  
 <213> Homo Sapiens

<400> 154  
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                          20                      25                      30  
 Glu Trp Val Glu Ser Ile Gly Gly Lys Val Pro Pro Ala Thr Gln Lys  
                          35                      40                      45  
 Ala Ile Ser Glu Glu Asn Thr Lys Glu Glu Lys Pro Asp Ser Lys Lys

50 55 60  
 Val Glu Glu Asp Leu Lys Ala Asp Glu Pro Ser Ser Glu Glu Ser Asp  
 65 70 75 80  
 Leu Glu Ile Asp Lys Glu Gly Val Ile Glu Pro Asp Thr Asp Ala Pro  
 85 90 95  
 Gln Glu Met Gly Asp Glu Asn Ala Glu Ile Thr Glu Glu Met Met Asp  
 100 105 110  
 Gln Ala Asn Asp Lys Lys Val Ala Ala Ile Glu Ala Leu Asn Asp Gly  
 115 120 125  
 Glu Leu Gln Lys Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn  
 130 135 140  
 Pro Arg Leu Ala Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys  
 145 150 155 160  
 Leu Gln Lys Pro Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu  
 165 170 175  
 Ile Asn Pro Asp Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His  
 180 185 190  
 Arg Leu Leu Gly His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala  
 195 200 205  
 Cys Lys Leu Asp Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val  
 210 215 220  
 Gln Pro Arg Ala Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg  
 225 230 235 240  
 Lys Arg Glu Glu Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys  
 245 250 255  
 Ala Arg Glu Glu His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg  
 260 265 270  
 Gln Ser Gly Ala Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly  
 275 280 285  
 Met Pro Gly Asn Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met  
 290 295 300  
 Pro Gly Met Ala Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro  
 305 310 315 320  
 Glu Val Leu Ala Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln  
 325 330 335  
 Asp Val Ala Gln Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro  
 340 345 350  
 Lys Val Met Asn Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln  
 355 360 365  
 Ala

<210> 155  
 <211> 1323  
 <212> DNA  
 <213> Homo Sapiens

<400> 155  
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 cagaaaagat ggaaaaaagg acatgtgcac tctgccccaa agatgtcgaa tataatgtcc 180  
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 gacttggtga atgtgaggat caggatccac ttaatcctga tagaagtttt gatgtggaat 300  
 cagtaaagaa agaaatccag agaggaagga agttgaaatg caaattttgt cataaaagag 360  
 gagccaccgt gggatgtgat ttaaaaaact gtaacaagaa ttaccacttt ttctgtgcca 420



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agaaggacga cgcagttcca cagtctgatg gagttcgagg aatttataaa ctgctttgcc 480
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aagttccttt tcttaagaaa tgcaaggga gaggacttc ttaattactt acttgaagaa 720
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aaa 1323

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&lt;210&gt; 156

&lt;211&gt; 191

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 156

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Met Glu Lys Arg Thr Cys Ala Leu Cys Pro Lys Asp Val Glu Tyr Asn
1          5          10          15
Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
20          25          30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
35          40          45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln
50          55          60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
65          70          75          80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
85          90          95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
100         105         110
Tyr Lys Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
115         120         125
Ser Ala Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
130         135         140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
145         150         155         160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
165         170         175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Gly Ser Arg Thr Ser
180         185         190

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&lt;210&gt; 157

&lt;211&gt; 4065

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 157

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gccagcaaag	agagtgatat	tgagcaattg	cgtgctaaac	ttttggacct	ctcggattct	3300
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tctttccgga aagtgggtcaa aaatacatct ggaaaaacta gttaa 4065

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&lt;210&gt; 158

&lt;211&gt; 1354

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 158

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Met Ser Thr Gly Asp Ser Phe Glu Thr Arg Phe Glu Lys Met Asp Asn
1      5      10      15
Leu Leu Arg Asp Pro Lys Ser Glu Val Asn Ser Asp Cys Leu Leu Asp
20     25     30
Gly Leu Asp Ala Leu Val Tyr Asp Leu Asp Phe Pro Ala Leu Arg Lys
35     40     45
Asn Lys Asn Ile Asp Asn Phe Leu Ser Arg Tyr Lys Asp Thr Ile Asn
50     55     60
Lys Ile Arg Asp Leu Arg Met Lys Ala Glu Asp Tyr Glu Val Val Lys
65     70     75     80
Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His Lys
85     90     95
Ser Thr Arg Lys Val Tyr Ala Met Lys Leu Leu Ser Lys Phe Glu Met
100    105    110
Ile Lys Arg Ser Asp Ser Ala Phe Phe Trp Glu Glu Arg Asp Ile Met
115    120    125
Ala Phe Ala Asn Ser Pro Trp Val Val Gln Leu Phe Tyr Ala Phe Gln
130    135    140
Asp Asp Arg Tyr Leu Tyr Met Val Met Glu Tyr Met Pro Gly Gly Asp
145    150    155    160
Leu Val Asn Leu Met Ser Asn Tyr Asp Val Pro Glu Lys Trp Ala Arg
165    170    175
Phe Tyr Thr Ala Glu Val Val Leu Ala Leu Asp Ala Ile His Ser Met
180    185    190
Gly Phe Ile His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
195    200    205
Ser Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asn
210    215    220
Lys Glu Gly Met Val Arg Cys Asp Thr Ala Val Gly Thr Pro Asp Tyr
225    230    235    240
Ile Ser Pro Glu Val Leu Lys Ser Gln Gly Gly Asp Gly Tyr Tyr Gly
245    250    255
Arg Glu Cys Asp Trp Trp Ser Val Gly Val Phe Leu Tyr Glu Met Leu
260    265    270
Val Gly Asp Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
275    280    285

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Lys Ile Met Asn His Lys Asn Ser Leu Thr Phe Pro Asp Asp Asn Asp  
 290 295 300  
 Ile Ser Lys Glu Ala Lys Asn Leu Ile Cys Ala Phe Leu Thr Asp Arg  
 305 310 315 320  
 Glu Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Lys Arg His Leu  
 325 330 335  
 Phe Phe Lys Asn Asp Gln Trp Ala Trp Glu Thr Leu Arg Asp Thr Val  
 340 345 350  
 Ala Pro Val Val Pro Asp Leu Ser Ser Asp Ile Asp Thr Ser Asn Phe  
 355 360 365  
 Asp Asp Leu Glu Glu Asp Lys Gly Glu Glu Glu Thr Phe Pro Ile Pro  
 370 375 380  
 Lys Ala Phe Val Gly Asn Gln Leu Pro Phe Val Gly Phe Thr Tyr Tyr  
 385 390 395 400  
 Ser Asn Arg Arg Tyr Leu Ser Ser Ala Asn Pro Asn Asp Asn Arg Thr  
 405 410 415  
 Ser Ser Asn Ala Asp Lys Ser Leu Gln Glu Ser Leu Gln Lys Thr Ile  
 420 425 430  
 Tyr Lys Leu Glu Glu Gln Leu His Asn Glu Met Gln Leu Lys Asp Glu  
 435 440 445  
 Met Glu Gln Lys Cys Arg Thr Ser Asn Ile Lys Leu Asp Lys Ile Met  
 450 455 460  
 Lys Glu Leu Asp Glu Glu Gly Asn Gln Arg Arg Asn Leu Glu Ser Thr  
 465 470 475 480  
 Val Ser Gln Ile Glu Lys Glu Lys Met Leu Leu Gln His Arg Ile Asn  
 485 490 495  
 Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys Arg Arg Asn Val  
 500 505 510  
 Glu Asn Glu Val Ser Thr Leu Lys Asp Gln Leu Glu Asp Leu Lys Lys  
 515 520 525  
 Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys Leu Ser Gln Leu Gln  
 530 535 540  
 Lys Gln Leu Glu Glu Ala Asn Asp Leu Leu Arg Thr Glu Ser Asp Thr  
 545 550 555 560  
 Ala Val Arg Leu Arg Lys Ser His Thr Glu Met Ser Lys Ser Ile Ser  
 565 570 575  
 Gln Leu Glu Ser Leu Asn Arg Glu Leu Gln Glu Arg Asn Arg Ile Leu  
 580 585 590  
 Glu Asn Ser Lys Ser Gln Thr Asp Lys Asp Tyr Tyr Gln Leu Gln Ala  
 595 600 605  
 Ile Leu Glu Ala Glu Arg Arg Asp Arg Gly His Asp Ser Glu Met Ile  
 610 615 620  
 Gly Asp Leu Gln Ala Arg Ile Thr Ser Leu Gln Glu Glu Val Lys His  
 625 630 635 640  
 Leu Lys His Asn Leu Glu Lys Val Glu Gly Glu Arg Lys Glu Ala Gln  
 645 650 655  
 Asp Met Leu Asn His Ser Glu Lys Glu Lys Asn Asn Leu Glu Ile Asp  
 660 665 670  
 Leu Asn Tyr Lys Leu Lys Ser Leu Gln Gln Arg Leu Glu Gln Glu Val  
 675 680 685  
 Asn Glu His Lys Val Thr Lys Ala Arg Leu Thr Asp Lys His Gln Ser  
 690 695 700  
 Ile Glu Glu Ala Lys Ser Val Ala Met Cys Glu Met Glu Lys Lys Leu  
 705 710 715 720  
 Lys Glu Glu Arg Glu Ala Arg Glu Lys Ala Glu Asn Arg Val Val Gln

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Asp Ile Asp Lys Leu Phe His Val Arg Pro Val Thr Gln Gly Asp Val  
 1170 1175 1180  
 Tyr Arg Ala Glu Thr Glu Glu Ile Pro Lys Ile Phe Gln Ile Leu Tyr  
 1185 1190 1195 120  
 Ala Asn Glu Gly Glu Cys Arg Lys Asp Val Glu Met Glu Pro Val Gln  
 1205 1210 1215  
 Gln Ala Glu Lys Thr Asn Phe Gln Asn His Lys Gly His Glu Phe Ile  
 1220 1225 1230  
 Pro Thr Leu Tyr His Phe Pro Ala Asn Cys Asp Ala Cys Ala Lys Pro  
 1235 1240 1245  
 Leu Trp His Val Phe Lys Pro Pro Pro Ala Leu Glu Cys Arg Arg Cys  
 1250 1255 1260  
 His Val Lys Cys His Arg Asp His Leu Asp Lys Lys Glu Asp Leu Ile  
 1265 1270 1275 128  
 Cys Pro Cys Lys Val Ser Tyr Asp Val Thr Ser Ala Arg Asp Met Leu  
 1285 1290 1295  
 Leu Leu Ala Cys Ser Gln Asp Glu Gln Lys Lys Trp Val Thr His Leu  
 1300 1305 1310  
 Val Lys Lys Ile Pro Lys Asn Pro Pro Ser Gly Phe Val Arg Ala Ser  
 1315 1320 1325  
 Pro Arg Thr Leu Ser Thr Arg Ser Thr Ala Asn Gln Ser Phe Arg Lys  
 1330 1335 1340  
 Val Val Lys Asn Thr Ser Gly Lys Thr Ser  
 1345 1350

<210> 159  
 <211> 683  
 <212> DNA  
 <213> Homo Sapiens

<400> 159  
 acaagctgga gttcgagcct gacagtggagg acaagatctc ggactgtgag gaaggattga 60  
 gtaatgtggc acttgaatgc agtgagccaa gcacaagtgt atctgtttat gaccagttga 120  
 aggcaccggc atccccctggg gctggaaacc cacctgggac cccaaaggga aagagagagc 180  
 tgatgagcaa tggcccagggt tccattattg gtgctaaagc tgggaagaat tctggcaaaa 240  
 agaagggcct taacaatgaa ctgaacaacc ttccagtaat ctccaacatg acggctgcgt 300  
 tagacagttg ctcggcagca gacggcagtt tggctgctga gatgcctaaa ctggaagcag 360  
 aaggattaat tgacaagaaa aatttaggag ataaagaaaa gggcaaaaaa gctaacaact 420  
 gcaaaacgga caaaaacctc tctaaactga aaagtgcctg gccattgcc cctgccccag 480  
 cccccactcc cccgcagcta atcgctatac ccaactgcaac ctttacaacg accaccactg 540  
 ggacaatacc cggactgccc tccctcacia caactgttgt tcaggctaca ccaaagagtc 600  
 ctccgttaaa acccattcaa ccaagccca caattatggg agagcccatc accgtgaacc 660  
 cagctctggg gtcactcaaa gac 683

<210> 160  
 <211> 227  
 <212> PRT  
 <213> Homo Sapiens

<400> 160  
 Lys Leu Glu Phe Glu Pro Asp Ser Glu Asp Lys Ile Ser Asp Cys Glu  
 1 5 10 15  
 Glu Gly Leu Ser Asn Val Ala Leu Glu Cys Ser Glu Pro Ser Thr Ser  
 20 25 30  
 Val Ser Ala Tyr Asp Gln Leu Lys Ala Pro Ala Ser Pro Gly Ala Gly

```

      35      40      45
Asn Pro Pro Gly Thr Pro Lys Gly Lys Arg Glu Leu Met Ser Asn Gly
  50      55      60
Pro Gly Ser Ile Ile Gly Ala Lys Ala Gly Lys Asn Ser Gly Lys Lys
  65      70      75      80
Lys Gly Leu Asn Asn Glu Leu Asn Asn Leu Pro Val Ile Ser Asn Met
      85      90      95
Thr Ala Ala Leu Asp Ser Cys Ser Ala Ala Asp Gly Ser Leu Ala Ala
  100      105      110
Glu Met Pro Lys Leu Glu Ala Glu Gly Leu Ile Asp Lys Lys Asn Leu
  115      120      125
Gly Asp Lys Glu Lys Gly Lys Lys Ala Asn Asn Cys Lys Thr Asp Lys
  130      135      140
Asn Leu Ser Lys Leu Lys Ser Ala Arg Pro Ile Ala Pro Ala Pro Ala
  145      150      155      160
Pro Thr Pro Pro Gln Leu Ile Ala Ile Pro Thr Ala Thr Phe Thr Thr
      165      170      175
Thr Thr Thr Gly Thr Ile Pro Gly Leu Pro Ser Leu Thr Thr Thr Val
      180      185      190
Val Gln Ala Thr Pro Lys Ser Pro Pro Leu Lys Pro Ile Gln Pro Lys
      195      200      205
Pro Thr Ile Met Gly Glu Pro Ile Thr Val Asn Pro Ala Leu Val Ser
      210      215      220
Leu Lys Asp
225

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<210> 161  
 <211> 662  
 <212> DNA  
 <213> Homo Sapiens

```

<400> 161
accacacagca gttgcacttg ctgagcaggc agcttgagga cccaaatggg agcttttcta      60
acgctgagat gagtgaactg agtgtggcac agaaaccaga aaaacttttg gagcgctgca      120
agtactggcc tgcttgtaaa aatgggggatg agtgtgccta ccatcacccc atctcacccct      180
gcaaagcctt cccaattgt aaatttgctg aaaaatgttt gtttgttcac ccaaattgta      240
aatatgtatg aaagtgtact aaaccagatt gtcctttcac tcatgtgagt agaagaattc      300
cagtactgtc tccaaaacca gttgcaccac cagcaccacc ttccagtagt cagctctgcc      360
gttacttccc tgcttgtaag aagatggaat gtcctttcta tcatccaaaa cattgttaggt      420
ttaacactca atgtacaaga cggactgca cattctacca tcccaccatt aatgtcccac      480
cacgacatgc cttgaaatgg attcgacctc aaaccagcga atagcaccca gtcctgacctg      540
gcagaagatc atgcagtttg gaagttttca tgtctgatga aagatctcta cagaacttgt      600
caaatctttg aaacttgga tatattgctt tcataatatg aagggtttatt ggctatctaa      660
aa

```

<210> 162  
 <211> 173  
 <212> PRT  
 <213> Homo Sapiens

```

<400> 162
Pro Gln Gln Leu His Leu Leu Ser Arg Gln Leu Glu Asp Pro Asn Gly
  1      5      10      15
Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro
      20      25      30

```

Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly  
                   35                  40                  45  
 Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro  
           50                  55                  60  
 Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys  
 65                  70                  75                  80  
 Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser  
                   85                  90                  95  
 Arg Arg Ile Pro Val Leu Ser Pro Lys Pro Val Ala Pro Pro Ala Pro  
                   100                  105                  110  
 Pro Ser Ser Ser Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met  
           115                  120                  125  
 Glu Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys  
           130                  135                  140  
 Thr Arg Pro Asp Cys Thr Phe Tyr His Pro Thr Ile Asn Val Pro Pro  
 145                  150                  155                  160  
 Arg His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu  
                   165                  170

<210> 163  
 <211> 2912  
 <212> DNA  
 <213> Homo Sapiens

<400> 163  
 cagttgcttc agcgtccccgg tgtggctgtg ccgttggtcc tgtgcggtca cttagccaag 60  
 atgcctgagg aaacccagac ccaagaccaa ccgatggagg aggaggaggt tgagacgttc 120  
 gcctttcagg cagaaattgc ccagttgatg tcattgatca tcaatacttt ctactcgaac 180  
 aaagagatct ttctgagaga gctcatttca aattcatcag atgcattgga caaaatccgg 240  
 tatgaaactt tgacagatcc cagtaaatta gactctggga aagagctgca tattaacctt 300  
 ataccgaaca aacaagatcg aactctcact attgtggata ctggaattgg aatgaccaag 360  
 gctgacttga tcaataacct tgggtactatc gccaaagtctg ggaccaaagc gttcatggaa 420  
 gctttgcagg ctggtgcaga tatctctatg attggccagt tcggtgttgg tttttattct 480  
 gcttatttgg ttgctgagaa agtaactgtg atcaccaaac ataacgatga tgagcagtac 540  
 gcttgggagt cctcagcagg gggatcattc acagtgagga cagacacagg tgaacctatg 600  
 ggctgtggaa caaaagttat cctacacctg aaagaagacc aaactgagta cttggaggaa 660  
 cgaagaataa aggagattgt gaagaaacat tctcagttta ttggatatcc cattactctt 720  
 tttgtggaga aggaacgtga taaagaagta agcgtgatg aggctgaaga aaaggaagac 780  
 aaagaagaag aaaaagaaaa agaagagaaa gagtccgaag acaaacctga aattgaagat 840  
 gttggttctg atgaggaaga agaaaagaag gatggtgaca agaagaagaa gaagaagatt 900  
 aaggaaaagt acatcgatca agaagagctc aacaaaacaa agcccatctg gaccagaaat 960  
 cccgacgata ttactaatga ggagtacgga gaattctata agagcttgac caatgactgg 1020  
 gaagatcact tggcagtga gcatTTTTtca gttgaaggac agttggaatt cagagccctt 1080  
 ctatttgtcc cagcagctgc tccttttgat ctgtttgaaa acagaaagaa aaagaacaat 1140  
 atcaaattgt atgtacgcag agttttcatc atggataact gtgaggagct aatccctgaa 1200  
 tatctgaact tcattagagg ggtggttagac tcggaggatc tccctctaaa catatcccgt 1260  
 gagatggttc aacaaagcaa aattttgaaa gttatcagga agaatttggc caaaaaatgc 1320  
 ttagaactct ttactgaact ggcggaagat aaagagaact acaagaaatt ctatgagcag 1380  
 ttctctaaaa acataaagct tggataacac gaagactctc aaaatcggaa gaagctttca 1440  
 gagctgttaa ggtactacac atctgcctct ggtgatgaga tggtttctct caaggactac 1500  
 tgcaccagaa tgaaggagaa ccagaaacat atctattata tcacagggtga gaccaaggac 1560  
 caggtagcta actcagcctt tgtggaacgt cttcggaac atggcttaga agtgatctat 1620  
 atgattgagc ccattgatga gtactgtgtc caacagctga aggaatttga ggggaagact 1680  
 ttagtgctcag tcaccaaaaga aggcctggaa cttccagagg atgaagaaga gaaaaagaag 1740  
 caggaagaga aaaaaacaaa gtttgagaac ctctgcaaaa tcatgaaaga catattggag 1800



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aaaaaagttg aaaaggtggt tgtgtcaaac cgattgggtga catctccatg ctgtattgtc 1860
acaagcacat atggctggac agcaaacatg gagagaatca tgaaaagctca agccctaaga 1920
gacaactcaa caatgggtta catggcagca aagaaacacc tggagataaa ccctgaccat 1980
tccattattg agaccttaag gcaaaaggca gaggtgata agaacgacaa gtctgtgaag 2040
gatctggtca tcttgcttta tgaaactgcg ctctgtctt ctggcttcag tctggaagat 2100
ccccagacac atgctaacag gatctacagg atgatcaaac ttggtctggg tattgatgaa 2160
gatgacccta ctgctgatga taccagtgtt gctgtaactg aagaaatgcc accccttgaa 2220
ggagatgacg acacatcacg catggaagaa gtagactaat ctctggctga gggatgactt 2280
acctgttcag tactctacaa ttctctgat aatataattt caaggatgtt tttctttatt 2340
tttgtaata ttaaaaagtc tgtatggcat gacaactact ttaaggggaa gataagattt 2400
ctgtctacta agtgatgctg tgatacctta ggcactaaag cagagctagt aatgcttttt 2460
gagtttcatg ttggttcttt cacagatggg gtaacgtgca ctgtaagacg tatgtaacat 2520
gatgttaact ttgtgtggtc taaagtgttt agctgtcaag ccggatgcct aagtagacca 2580
aatcttgtaa ttgaagtgtt ctgagctgta tcttgatgtt tagaaaagta ttcgttacat 2640
ctttaggat ctactttttg aacttttcat tccctgtagt tgacaattct gcatgtacta 2700
gtcctctaga aatagggttaa actgaagcaa cttgatggaa ggatctctcc acagggttg 2760
tttccaaag aaaagtattg ttggaggag caaagttaaa agcctaccta agcatatcgt 2820
aaagctgttc aaatactcga gccagtcct gtggatggaa atgtagtgct cgagtcacat 2880
tctgcttaaa gttgtaacaa atacagatga gt 2912

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&lt;210&gt; 164

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 164

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Met Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu
1      5      10      15
Val Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu
20      25      30
Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu
35      40      45
Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Thr Leu
50      55      60
Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu
65      70      75      80
Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
85      90      95
Gly Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys
100     105     110
Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile
115     120     125
Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val
130     135     140
Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
145     150     155     160
Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
165     170     175
Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
180     185     190
Asp Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
195     200     205
Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
210     215     220
Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp

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Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg Ile  
 675 680 685  
 Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro Thr  
 690 695 700  
 Ala Asp Asp Thr Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu Glu  
 705 710 715 720  
 Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp  
 725 730

&lt;210&gt; 165

&lt;211&gt; 790

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 165

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ccgactcaga aatggcgggc tccatgttct acggcaggct agtggccgtg gccacccttc      60
ggaaccaccg gcctcggaag gccacggggg ctgctgtctca ggttctggga agttctggat      120
tgtttaataa ccatggactc caagtacagc agcaacagca aaggaatctc tcactacatg      180
aatacatgag tatggaatta ttgcaagaag ctggtgtctc cgttcccaaa ggatatgtgg      240
caaagtcacc agatgaagct tatgcaattg ccaaaaaaatt aggttcaaaa gatgtcgtga      300
taaaggcaca ggttttagct ggtggtagag gaaaaggaac atttgaaagt ggcctcaaag      360
gaggagtga gtagttttct tctccagaag aagcaaaagc tgtttcttca caaatgattg      420
ggaaaaaatt gtttaccaag caaacgggag aaaagggcag aatatgcaat caagtattgg      480
tctgtgagcg aaaatatccc aggagagaat actactttgc aataacaatg gaaaggtcat      540
ttcaagggtcc tgtattaata ggaagttcac atggtggtgt caacattgaa gatgttgctg      600
ctgagtctcc tgaagcaata attaaagaac ctattgatat tgaagaaggc atcaaaaagg      660
aacaagctct tcagcttgca cagaagaatg ggatttcccc taatattgng ggaatcagca      720
gcaggaaaac atggtcaagc tttacagncn ttttcttgaa atacgatgca acccttgata      780
ggaaattaaa                                     790

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&lt;210&gt; 166

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 166

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Asp Ser Glu Met Ala Ala Ser Met Phe Tyr Gly Arg Leu Val Ala Val
  1           5           10           15
Ala Thr Leu Arg Asn His Arg Pro Arg Thr Ala Gln Arg Ala Ala Ala
  20           25           30
Gln Val Leu Gly Ser Ser Gly Leu Phe Asn Asn His Gly Leu Gln Val
  35           40           45
Gln Gln Gln Gln Gln Arg Asn Leu Ser Leu His Glu Tyr Met Ser Met
  50           55           60
Glu Leu Leu Gln Glu Ala Gly Val Ser Val Pro Lys Gly Tyr Val Ala
  65           70           75           80
Lys Ser Pro Asp Glu Ala Tyr Ala Ile Ala Lys Lys Leu Gly Ser Lys
  85           90           95
Asp Val Val Ile Lys Ala Gln Val Leu Ala Gly Gly Arg Gly Lys Gly
  100          105          110
Thr Phe Glu Ser Gly Leu Lys Gly Gly Val Lys Ile Val Phe Ser Pro
  115          120          125
Glu Glu Ala Lys Ala Val Ser Ser Gln Met Ile Gly Lys Lys Leu Phe
  130          135          140
Thr Lys Gln Thr Gly Glu Lys Gly Arg Ile Cys Asn Gln Val Leu Val

```

145		150		155		160									
Cys	Glu	Arg	Lys	Tyr	Pro	Arg	Arg	Glu	Tyr	Phe	Ala	Ile	Thr	Met	
			165					170					175		
Glu	Arg	Ser	Phe	Gln	Gly	Pro	Val	Leu	Ile	Gly	Ser	Ser	His	Gly	Gly
			180					185					190		
Val	Asn	Ile	Glu	Asp	Val	Ala	Ala	Glu	Ser	Pro	Glu	Ala	Ile	Ile	Lys
		195					200					205			
Glu	Pro	Ile	Asp	Ile	Glu	Glu	Gly	Ile	Lys	Lys	Glu	Gln	Ala	Leu	Gln
	210					215					220				
Leu	Ala	Gln	Lys	Asn	Gly	Ile	Ser	Pro	Asn	Ile	Gly	Ile	Ser	Ser	Arg
225				230					235					240	
Lys	Thr	Trp	Ser	Ser	Phe	Thr	Phe	Leu	Lys	Tyr	Asp	Ala	Thr	Leu	Asp
			245					250						255	
Arg	Lys	Leu													

<210> 167  
 <211> 5307  
 <212> DNA  
 <213> Homo Sapiens

<400> 167

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ggtgctccta	atccctgtgt	tgttaaaggg	tcgactatat	tgtatttttg	aaaattgcta	120
gagagtggac	gtaaagtgtt	ctcactaaac	aaattataac	tatgtgaggt	agtgcataata	180
ttaaagtagct	agatttgggc	attccacaat	gtatatgtac	ttcaaaacat	catgttgtac	240
atgagaaaca	cagttttatc	tgttagtcag	ttttaaaaat	aaaaaatatt	ccaactagaa	300
actctgttgt	agtttttgaa	attacaactt	ggaggctttg	aggaactgat	tagaagtctc	360
ctttctgttt	caggctttca	tatccaaacc	atagatcttt	agaagtaaca	tctgttaatt	420
aattattaat	aaatagtttg	agtctttatt	aattcatgga	taacttgacc	atcttctctc	480
tccttttgc	tagataatcc	cagatcatgg	ccgggcacag	tagctcacgc	ctgtattccc	540
agcagtttgg	gaggccgagg	caggcagatc	acttgaactc	aggagtttga	gaccagcttg	600
ggcaacatgg	caaaaccctg	tctctattaa	aaatacaaaa	attagctggg	catggtagtg	660
catgcctgta	gtcccagcta	cctgggaggc	tgagggtggga	ggatcgcttg	agcctgggag	720
gttgaggcct	ctgtgcgcga	tgattgctcc	agtgatcacg	ccattgcact	ccagcctggg	780
tgacagagtg	agaccctgtc	tccaaaaaaa	aaaaaaatta	agcaagtagc	agttacaaga	840
ccaaaagtta	ttttcctttt	ttttttctc	tataaaattg	cccatttgga	ccaaatctag	900
ttataactta	tttcagtgtc	attaagaaa	ttgatgaata	agtcataatta	ctcagatgtt	960
agtagctatg	catttattaa	tagttttatt	tataagtatt	tagtttcact	ctgttgacga	1020
ctattttatg	ctaaaattag	ctaaagccaa	attactattt	cttaaaacat	atcttttact	1080
tttttttttt	ttttaaatat	tattaggtac	ttcttgcaag	ggatatgcat	tagcacatac	1140
tcaagaagg	gaagaaaaga	agcaaaactc	tggtacatca	aataccagag	gatcaagaag	1200
aaaacctgca	atgacaactc	ctacaaggag	gtctacacgt	aacacaagag	ctgaaacagc	1260
cagtcagctc	cagagatccc	caatatcaga	caattctggg	tgtgatgccc	caggtaacag	1320
taatccatct	ttaagtgttc	cctcttcagc	tgagtcagaa	aagcaaaca	gacaggctcc	1380
aaaacggaag	tctgtaagaa	gaggaagaaa	accaccttta	ctgaaaaaga	aacttcggag	1440
ctctgtagct	gcccctgaaa	aatcatcttc	caatgattca	gtagatgaag	aaacagcaga	1500
atctgacaca	tcacctgtgt	tagaaaaaga	gcaccaacca	gatgtagaca	gtagtaacat	1560
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5307

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 <211> 1148  
 <212> PRT  
 <213> Homo Sapiens

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 50 55 60  
 Gly Arg Lys Pro Pro Leu Leu Lys Lys Lys Leu Arg Ser Ser Val Ala  
 65 70 75 80  
 Ala Pro Glu Lys Ser Ser Ser Asn Asp Ser Val Asp Glu Glu Thr Ala  
 85 90 95  
 Glu Ser Asp Thr Ser Pro Val Leu Glu Lys Glu His Gln Pro Asp Val  
 100 105 110  
 Asp Ser Ser Asn Ile Cys Thr Val Gln Thr His Val Glu Asn Gln Ser  
 115 120 125  
 Ala Asn Cys Leu Lys Ser Cys Asn Glu Gln Ile Glu Glu Ser Glu Lys  
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 His Thr Ala Asn Tyr Asp Thr Glu Glu Arg Val Gly Ser Ser Ser Ser  
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 Glu Ser Cys Ala Gln Asp Leu Pro Val Leu Val Gly Glu Glu Gly Glu  
 165 170 175  
 Val Lys Lys Leu Glu Asn Thr Gly Ile Glu Ala Asn Val Leu Cys Leu  
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 Glu Ser Glu Ile Ser Glu Asn Ile Leu Glu Lys Gly Gly Asp Pro Leu  
 195 200 205  
 Glu Lys Gln Asp Gln Ile Ser Gly Leu Ser Gln Ser Glu Val Lys Thr  
 210 215 220  
 Asp Val Cys Thr Val His Leu Pro Asn Asp Phe Pro Thr Cys Leu Thr  
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 Gly His Val Glu Thr Glu Asp Val Glu Ile Ile Ala Thr Cys Asp Thr  
 325 330 335  
 Phe Gly Asn Glu Asp Phe Asn Asn Ile Gln Asp Ser Glu Asn Asn Leu  
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Met Ile Pro Met Glu Cys Asp Ser Phe Cys Ser Asp Gln Asn Glu Ser		400
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Asp Glu Lys Val Glu Thr Val Ser Gln Pro Ser Glu Ser Pro Lys Asp		
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Asn Asp Gly Trp Arg Cys Pro Arg Gly Asn Asp Arg Tyr Arg Lys Asn		
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Asp Pro Glu Lys Gln Asn Glu Asn Thr Arg Lys Glu Lys Asn Asp Ile		
675	680	685
His Leu Asp Ala Asp Asp Pro Asn Ser Ala Asp Lys His Arg Asn Asp		
690	695	700
Cys Pro Asn Trp Ile Thr Glu Lys Ile Asn Ser Gly Pro Asp Pro Arg		
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Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu Glu Asn Arg		
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Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly Ser Gly Trp		
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Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg Trp Gln Asn		
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<211> 597
<212> DNA
<213> Homo Sapiens
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acttqqatca	agttccctcc	cctctcctca	aaatatatcg	acttgtgtctg	aaagaaatca	240



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&lt;210&gt; 170

&lt;211&gt; 3344

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 170

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&lt;210&gt; 171

&lt;211&gt; 1004

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 171

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Ser Ala Thr Ile Pro Leu Asp Asp Pro Thr Leu Leu Phe Ala Asn Ala
65     70     75     80
Gly Met Asn Gln Phe Lys Pro Ile Phe Leu Asn Thr Ile Asp Pro Ser
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His Pro Met Ala Lys Leu Ser Arg Ala Ala Asn Thr Gln Lys Cys Ile
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Gln Tyr Asn Arg Glu Ala Asp Gly Ile Leu Lys Pro Leu Pro Lys Lys
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 Val Pro Val Ser Glu Leu Leu Asp Asp Pro Ser Gly Pro Ala Gly Ser  
 740 745 750  
 Leu Thr Ser Val Glu Phe Cys Gly Gly Thr His Leu Arg Asn Ser Ser  
 755 760 765  
 His Ala Gly Ala Phe Val Ile Val Thr Glu Glu Ala Ile Ala Lys Gly  
 770 775 780  
 Ile Arg Arg Ile Val Ala Val Thr Gly Ala Glu Ala Gln Lys Ala Leu  
 785 790 795 800  
 Arg Lys Ala Glu Ser Leu Lys Lys Cys Leu Ser Val Met Glu Ala Lys  
 805 810 815  
 Val Lys Ala Gln Thr Ala Pro Asn Lys Asp Val Gln Arg Glu Ile Ala  
 820 825 830  
 Asp Leu Gly Glu Ala Leu Ala Thr Ala Val Ile Pro Gln Trp Gln Lys  
 835 840 845  
 Asp Glu Leu Arg Glu Thr Leu Lys Ser Leu Lys Lys Val Met Asp Asp  
 850 855 860  
 Leu Asp Arg Ala Ser Lys Ala Asp Val Gln Lys Arg Val Leu Glu Lys  
 865 870 875 880  
 Thr Lys Gln Phe Ile Asp Ser Asn Pro Asn Gln Pro Leu Val Ile Leu  
 885 890 895  
 Glu Met Glu Ser Gly Ala Ser Ala Lys Ala Leu Asn Glu Ala Leu Lys  
 900 905 910  
 Leu Phe Lys Met His Ser Pro Gln Thr Ser Ala Met Leu Phe Thr Val  
 915 920 925  
 Asp Asn Glu Ala Gly Lys Ile Thr Cys Leu Cys Gln Val Pro Gln Asn  
 930 935 940  
 Ala Ala Asn Arg Gly Leu Lys Ala Ser Glu Trp Val Gln Gln Val Ser  
 945 950 955 960  
 Gly Leu Met Asp Gly Lys Gly Gly Gly Lys Asp Val Ser Ala Gln Ala  
 965 970 975  
 Thr Gly Lys Asn Val Gly Cys Leu Gln Glu Ala Leu Gln Leu Ala Thr  
 980 985 990  
 Ser Phe Ala Gln Leu Arg Leu Gly Asp Val Lys Asn  
 995 1000

&lt;210&gt; 172

&lt;211&gt; 659

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 172

gcctgagcaa	cgtctccgag	caggcgctgg	gctagaggcg	ggtctcaacc	agctactcat	60
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gaaccaaccg	agtcggatcc	tgaccctaaa	acctagtatt	ttccacttgt	tcataaatat	180
ggaaaactca	gattccaatg	acaaaggaag	tggtgatcag	tctgcagcac	agcgcagaag	240
tcagatggac	cgattggatc	gagaagaagc	tttctatcaa	tttgtaaata	acctgagtga	300
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ggaagagttg	ctgagacgac	tacagcaaat	taaagaaggc	ccaccaccgc	aaaactcaga	420
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gcttaactct	gtcagacaaa	ctggaaatac	aacaagaagt	gggcaaagag	gaaaccaatc	540
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<210> 173  
 <211> 192  
 <212> PRT  
 <213> Homo Sapiens

<400> 173  
 Pro Glu Gln Arg Leu Arg Ala Gly Ala Gly Leu Glu Ala Gly Leu Asn  
 1 5 10 15  
 Gln Leu Leu Ile Gly Gly Gly Leu Glu Ser Gly Gly Gln Gly Gly Ala  
 20 25 30  
 Glu Gln Pro Arg Arg Arg Arg Pro Asn Gln Pro Ser Arg Ile Leu Thr  
 35 40 45  
 Leu Lys Pro Ser Ile Phe His Leu Phe Ile Asn Met Glu Asn Ser Asp  
 50 55 60  
 Ser Asn Asp Lys Gly Ser Gly Asp Gln Ser Ala Ala Gln Arg Arg Ser  
 65 70 75 80  
 Gln Met Asp Arg Leu Asp Arg Glu Glu Ala Phe Tyr Gln Phe Val Asn  
 85 90 95  
 Asn Leu Ser Glu Glu Asp Tyr Arg Leu Met Arg Asp Asn Asn Leu Leu  
 100 105 110  
 Gly Thr Pro Gly Glu Ser Thr Glu Glu Glu Leu Leu Arg Arg Leu Gln  
 115 120 125  
 Gln Ile Lys Glu Gly Pro Pro Gln Asn Ser Asp Glu Asn Arg Gly  
 130 135 140  
 Gly Asp Ser Ser Asp Asp Val Ser Asn Gly Asp Ser Ile Ile Asp Trp  
 145 150 155 160  
 Leu Asn Ser Val Arg Gln Thr Gly Asn Thr Thr Arg Ser Gly Gln Arg  
 165 170 175  
 Gly Asn Gln Ser Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Ser Gly  
 180 185 190

<210> 174  
 <211> 610  
 <212> DNA  
 <213> Homo Sapiens

<400> 174  
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 tggctcttggtg gacagtagtt tgcccacagt tgggtgttttt gcaaaaagcaa ctgcacaaga 120  
 caaccccaaa tctgccacag agcagtcagg aactggatc cgatcagaga gtgagacaga 180  
 gtccgaggcc tcagaaatta ctattcctcc cagcaccocg gcagttccac aggcctcccg 240  
 ccagggggag gactacggca aaggtgtcat cttctacctc agggacaaag tggctcgtggg 300  
 gattgtgcta tggaacatct ttaaccgaat gccaatagca aggaagatca ttaaggacgg 360  
 tgagcagcat gaagatctca atgaagtagc caaactattc aacattcatg aagactgaag 420  
 cccacagtg gaattggcaa acccactgca gcccttgaga ggaggtcgaa tgggttaaagg 480  
 agcatttttt tattcagcag actttctctg tgtatgagtg tgaatgatca agtcctttgt 540  
 gaatattttc aactatgtag gtaaattctt aatgttcnca tagtgaaata aattctgatt 600  
 cttctaaaaa 610

<210> 175  
 <211> 138  
 <212> PRT  
 <213> Homo Sapiens

<400> 175

Tyr Trp His Gln Ser Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly  
 1 5 10 15  
 Tyr Glu Ala Ile Gly Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val  
 20 25 30  
 Phe Ala Lys Ala Thr Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln  
 35 40 45  
 Ser Gly Thr Gly Ile Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser  
 50 55 60  
 Glu Ile Thr Ile Pro Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val  
 65 70 75 80  
 Gln Gly Glu Asp Tyr Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys  
 85 90 95  
 Val Val Val Gly Ile Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile  
 100 105 110  
 Ala Arg Lys Ile Ile Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu  
 115 120 125  
 Val Ala Lys Leu Phe Asn Ile His Glu Asp  
 130 135

<210> 176  
 <211> 805  
 <212> DNA  
 <213> Homo Sapiens

<400> 176  
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 ctggccaaga cctgccctgt gcagctgtgg gttgattcca ccccccgcc cggcaccgcg 120  
 gtccgcgcca tggccatcta caagcagtc cagcacatga cggaggttgt gaggcgctgc 180  
 ccccaccatg agecgtgctc agatagcgat ggtctggccc ctctcagca tcttatccga 240  
 gtggaaggaa atttgcgtgt ggagtatttg gatgacagaa acacttttgc acatagtgtg 300  
 gtggtgccct atgagccgcc tgaggttggc tctgactgta ccaccatcca ctacaactac 360  
 atgtgtaaca gttcctgcat gggcggcatg aaccggaggc ccaccctcac catcatcaca 420  
 ctggaagact ccagtggtaa tctactggga cggaacagct ttgaggtgcg tgtttgtgcc 480  
 tgtcctggga gagaccggcg cacagaggaa gagaatctcc gcaagaaagg ggagcctcac 540  
 cacgaagctg cccccaggga gcactaagcg agcactgccc aacaacacca agctcctctc 600  
 cccagccaaa gaagaaancca ctggatngag aatatttcac cccttcanat tcgttgggcg 660  
 tgagcgcttc cganaatgtt ccgaagagct gnaagaaggc cttgggaact caaaggatgc 720  
 ccaaggcttg ggaaaggagc caangggggg gaancaangg gctcaactnc aagccaacct 780  
 gaaagttcca aaaaanggtt ccagt 805

<210> 177  
 <211> 626  
 <212> DNA  
 <213> Homo Sapiens

<400> 177  
 ctaatttgtc tgtttattcc cacaaggtag ccaggggtgg gggcgccgag ccaagcccag 60  
 caggccatgg gaccttctc cggcggggtg cagctggat ttccgggtct gccccaccag 120  
 caggtttgca ggcaggcgt catgagtgc ggtggaaggc tccgagggcg tgggcagggg 180  
 ctccggcggg gccacacact tgtggagcta gaaatantgg ggcaggctct tctctatcac 240  
 caggggctcc tccatgggtc cgtagcgctt caccacgcag ccgttcttgt cgatgaggaa 300  
 ctgtgganan acggtgtcca aactgtgggg ccacccctgc aaggggctga ggctgccctt 360  
 cctgtccgct gcccatctgg gccacggctg tggccagggg aaactggctc cctaccccc 420  
 acagccccct tacctttggt gaagttccac ttgatggcac tggaaaanaa gcacatggac 480  
 gtgagcgtcc ccaggcagcc cccacagtc cccaaagctt gtccctgtctc caaggaggcc 540

anaaaggttg tnagcttccc cgggtncctc cacangccac agtgcccca aanccccc 600  
 aanagccatc tttaccccaa ggaggg 626

<210> 178  
 <211> 793  
 <212> DNA  
 <213> Homo Sapiens

<400> 178  
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 gcggcgggccc ctcttatgct gggaggatgc tggagagtag cggctgcaaa gcgctgaagg 120  
 agggcggtgct ggagaagcgc agcgacgggt tgttgcaact ctggaagaaa aagtgttgca 180  
 tcctcaccga ggaagggctg ctgcttatcc cgcacaagca gctgcaaac cagcagcagc 240  
 agcaacagca gcagcagcag cagcaacaac agcccgggca ggggcgggcc gagccgtccc 300  
 aacccagtgg ccccgctgtc gccagcctcg agccgcgggt caagctcaag gaactgcact 360  
 tctccaacat gaagaccgtg gactgtgtgg agcgcaaggg caagtacatg tacttcactg 420  
 tgggtgatggc agaggggcaag gagatcgact ttcgggtgccc gcaagaccag ggctggaacg 480  
 ccgagatcac gctgcagatg gtgcagtaca agaatcgta ggccatcctg gcggtcaaact 540  
 ccacgcggca gaagcagcag cacctggtcc agcancagcc cccctcgag ccgcagccgc 600  
 agccgcagct ccaagcccca acccagcct tcagcctcaa gcngcaacc ccaagcccca 660  
 attcacaac ccaagccct caagcccaa cccaaagccc tcangccca ngcaagntcc 720  
 aaccggttat ncggccatcc aacattcaan atccaanact ctcaangcct taactnccn 780  
 acccaanaac nct 793

<210> 179  
 <211> 786  
 <212> DNA  
 <213> Homo Sapiens

<400> 179  
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 agtactcgag aaataatgaa taaattctta atgttttccc ctccaccgcc cttttttatt 120  
 ctccaagatt aggaattact acggattagg tttttgaaaa taaagtttcc tttttggaaa 180  
 atggtctaca ttcagaaatg tcttagaaca agcattttaa aaaaactaat aaataatcat 240  
 aaatcaaaat acattaaaat aaaattacag tacatcatcg ctccatagaaa attcaccata 300  
 caagacgatc ctttcaaagg ttcataaata aaagtcttct tgactcgaaa tcgtttcctg 360  
 catcgtgatg aaaagtatgc agaaaactaa gaagaatcgc aagttttcag taggggtgatg 420  
 tccaaactac ttgatctggt gcggggcgga gagactgttt tgcttttgat ccaagtgaag 480  
 acaatagaaa tgtgctcgtc ccacttcctc aagtcctcaa aaccttgtct tgcccgagg 540  
 ctgccccctt cangcagagt tgggaggtgc tgcgganaaa ccggtgccc tgccggtgcc 600  
 aatgcggctg tgggtgtggg tgcngtattt ggtgcgggat gcnggtgcc ggtnaaggtg 660  
 tggggtgcca antnaaggat gaaaatgtgg atnttngnat nttgattccg gatacggggt 720  
 gggaacctng cngggggccn naaggcttgg ggttggggct naanggctgg ggttttttaa 780  
 ttgggg 786

<210> 180  
 <211> 791  
 <212> DNA  
 <213> Homo Sapiens

<400> 180  
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 aggaggggat cctgcagctg cgtgcacca actcagccaa gccagtgcca ctggcaccat 120  
 cctcatggc ctcttctccg acttctatct gtgtgtgtgg gcaggtgcca gctgggggtg 180  
 gagttctgca gtgtgacctg tgtcaggact ggttccatgg gcagtgtgtg tcagtgtccc 240

atctcctcac	ctctccaaag	cccagttctca	cttcatctcc	actgctagcc	tggtgggaat	300
gggacacaaa	attcctgtgt	ccactgtgta	tgcgctcacg	acggccacgc	ctagagacaa	360
tcctagcctt	gctgggtgcc	ctgcagaggc	tgcccgtgcg	gctgcctgag	ggtgaggccc	420
ttcagtgtct	cacagagagg	gccattgggt	ggcaagaccg	tgccagaaaag	gctctggcct	480
ctgaagatgt	gactgctctg	ttgcgacagc	tggtctgagct	tcgccaacag	ctacaggcca	540
aacccanacc	agaggaggcc	tcagtctaca	cttcagccac	tgccctgtgac	cctatcagag	600
aaggcagtgg	caacaatatt	tcnaangtcc	aagggtctgct	ggagaatgga	gacantgttg	660
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cctggaggga	g					791

<210> 181  
 <211> 747  
 <212> DNA  
 <213> Homo Sapiens

<400> 181						
agtatccaaa	catactcatt	gtttttat	ttt taacaaaaga	aatgaaatta	aagatagacc	60
acaggtagag	tcattgaaatt	cttggtttt	tc cctattcttt	ttggttaatta	caacgtacat	120
tgtcttcttt	tataataaga	cccaagggga	gaaaagaaaa	ggatgtacaa	tgaagggtaca	180
agttttgaag	cacccaaaata	ttttatgaca	gggacaaaaa	aacaaaaaac	aaacaaaaat	240
tgaagtacag	aaagaggggtg	gtgggggcaa	aaataaaggt	acgcacttgg	gcttctctcaa	300
gattttgtttg	tccttattca	gactagaatg	aaactggttt	aggaaatcac	tcctgtatgc	360
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ccttttaaca	gtaactctag	gagagaggat	atcaaaaatt	ggcagtgaaa	aattatagat	480
aggcaaaaag	ctccttctga	ggtccaggcc	aggagatagt	angattttaag	aaacaaacaa	540
acaataacaa	ccacaaatgg	acctttgggt	ccactgtcac	aactgttgct	catcagagta	600
ggagaattgt	ancaaaggca	ttaaagaagg	gacaagcaag	ctgaagagcc	tgaatccttg	660
gggttgtaag	cenatttttg	gnttcctttc	aagaaaaggg	ctgttggnccg	gtggaanggg	720
tcanggaaca	ntatttcacg	ggtcngc				747

<210> 182  
 <211> 909  
 <212> DNA  
 <213> Homo Sapiens

<400> 182						
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tgctcaatga	aataaaaagag	gatacaaaaca	aatggaagaa	cattccatgc	tcattgggtag	180
gaagaatcaa	tatcgtgaaa	atggccatac	tgcccaaggt	aatgtataga	ttcaatgcca	240
tccccatcaa	gctaccaatg	actttcttca	cagaatttga	aaaaactact	caaaagtcca	300
tatggaacca	aaaaagagcc	cacattgcca	agtcaatcct	aagccaaaag	aacaaagctg	360
gaggcatcac	gctacctgac	ttcaaactat	actacaaggc	tacagtaacc	aaaacagcgt	420
ggtactggta	ccaaaacaga	gatataaatc	aatgcaacag	aacagagccc	tcagaaataa	480
tgccacatat	ctacaactat	ctgatctttg	acaaacctga	gaaaaacaag	caatggggaa	540
aggattccct	atttaataaa	tggtgctggg	aaaactggct	agccatatgt	agaaagctga	600
aactggatct	cttctttata	ccttatacaa	aaattaattg	aagatggntt	aaaggactta	660
aacgttagac	ctaaaaccat	aaaaacccta	gaagaaaaac	ctaggcatta	ccattcangg	720
acataggctt	gggcaaggac	ttcctgtcta	aaacaccaan	agcaatggga	ncaaaagcca	780
aaattgcaaa	tggggattct	aattaaactaa	agggcttttg	cacagcnaag	aagctccatc	840
agagngaaca	ggaacntcaa	antgggagaa	attttgaacc	taccatcnga	naaggctaata	900
nccagaatc						909

<210> 183



&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 183

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tctcctaagt	ctatccctcc	cgctccccc	caccccacaa	cagtccccag	agtgtgatgt	180
tccccttcct	gtgtccatgt	gttctcactg	ttcaattccc	acctatgagt	gagaatatgc	240
gggtgttggt	ttttttgtcc	ttgccatagt	ttactgagaa	tgatgatttc	caatttcac	300
cctgtcccta	caaaggacat	gaactcatca	ttttttatgg	ctgcatagta	ttccatgggtg	360
tatatgtgcc	acattttctt	aatccagtct	atcattgttg	gccatttggg	ttggttccaa	420
gtctttgcta	ttgtgaatac	tgccgcaata	aacatacgtg	tgcatgtgtc	tttatagcag	480
catgatttat	antcctttgg	gtatatactc	agtaatggga	tggctgggtc	aaatgggnatt	540
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gtcccancaa	cagngtnaaa	gggtccnaan	tcnccaaaat	cctctccaag	caccngttgt	660
tcccggactt	tttaanggat	tncaattcc	aaccggngt	caaaagg		708

&lt;210&gt; 184

&lt;211&gt; 855

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 184

agactcacag	tctgctggtg	ggcagagaag	acagaaacga	catgagcaca	gcaggaaaag	60
taatcaaatg	caaagcagct	gtgctatggg	aggtaaagaa	acccttttcc	attgaggatg	120
tggaggttgc	acctcctaag	gcttatgaag	ttcgcattaa	gatggtggct	gtaggaatct	180
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gccatgaggc	agccggcatc	gtggagagt	ttggagaagg	ggtgactaca	gtcaaacccag	300
gtgataaagt	catcccgctc	ttactcctc	agtgtggaaa	atgcagagtt	tgtaaaaacc	360
cggagagcaa	ctactgcttg	aaaaatgatc	taggcaatcc	tcgggggacc	ctgcaggatg	420
gcaccaggag	gttcacctgc	agggggaagc	ccattcacca	cttccttggc	accagcacct	480
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gttgccaagg	tcaccccagg	ctctacctgt	gctgtgtgtg	gcctgggaag	ggtcggccta	660
tctgctgtta	tgggctgtta	aagcaactgg	aggcanccag	aatcaattgc	ggtggacatc	720
aacaaggaca	aattttgcaa	agggcaaaaag	agttgggtgc	cactgaatgc	catcaaccct	780
caagnctnca	ngnaaaccca	tccaggnaag	tgctaaaang	gaatttaccg	attggaggggt	840
ttggattttt	ccgtt					855

&lt;210&gt; 185

&lt;211&gt; 865

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 185

cacagatgtt	caatcaactg	atgaagcaag	tgctcaggact	tactgttgac	acagaggagc	60
ggctgaaagg	agttattgac	ctggtctttg	agaaggctat	tgatgaaccc	agttttctctg	120
tggcttacgc	aaacatgtgt	cgatgtctag	taacgctgaa	agtacccatg	gcagacaagc	180
ctggtaacac	agtgaatttc	cggaaagctgc	tactgaaccg	tgccagaag	gagtttgaaa	240
aagataaagc	agatgatgat	gtcttttgaga	agaagcagaa	agaacttgag	gctgccagt	300
ctccagagga	gaggacaagg	cttcatgatg	aactggaaga	agccaaggac	aaagcccggc	360
ggagatccat	tggcaacatc	aagttttattg	gagaactctt	taaactcaaa	atgctgactg	420
aagccatcat	gcatgactgt	gtgggtgaagc	tgctaaagaa	ccatgatgaa	gaatccctgg	480
agtgcctgtg	tcgcctgtct	accaccattg	gcaaagactt	ggactttgaa	aaagcaaagc	540

cacgtatgga	ccagtacttt	aatcaagatg	gagaaaattg	tnaaagaaag	aaaaacctca	600
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atctcgaaag	agcagatnaa	gggcctnaan	ctatcgaaca	gattcacaaa	ganggctaaa	720
attgaaanaa	caagaatagc	caaaggggaag	gnccaacaac	tcattggacca	anggagaaat	780
agaataccaa	ggtgttccaa	aaanttggcc	aaangnnggt	tggaaanaacn	gttcaaaggg	840
ggccangaaa	aantccgggt	actgg				865

&lt;210&gt; 186

&lt;211&gt; 736

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 186

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agagtacttt	tctcagggtg	gcactttngt	ttttttaaac	aattcttggg	gttctgtggg	120
ccacagcatt	tccttctgtt	tcaatgttat	gtatgttttg	attactattg	tgatttttta	180
aattttctga	agcaagctga	gaggcaggca	gaaagatttg	atgccaaaaa	aaaaaaaaatc	240
tttcttacct	tggtcacccc	aaactttctc	aaatctggac	taaatgctat	accttaaaac	300
aaacatgagg	tgcatcttga	aggggaggga	aatttatttc	tctgcttttc	tattatacaa	360
gttgtttaca	gaaactgcaa	attaaaaaat	tacactggca	tttgcatgcc	ttaaaaataaa	420
ttaaaaagttc	tcaacttttt	tttttttttg	ctaaacattt	ttttaagtat	gagtccttgt	480
ttaaaaagaa	aagattaaaa	cagaaaaatat	tttctataaa	taatacatgt	attttggttt	540
tagtgctccc	gccctaagg	ttgaagttta	cttttancca	ngtacctttt	tcctccatga	600
tcaccttttt	ttctctttcc	cctctcccaa	ntcctgtcac	acgtgggggt	ttccggcaan	660
aattggcctt	gctgnactgt	gattgggcga	anaacgttga	aaaacctttt	taaaaaaaaa	720
tacttaaaat	tgggtt					736

&lt;210&gt; 187

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 187

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&lt;210&gt; 188

&lt;211&gt; 802

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 188

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&lt;210&gt; 189

&lt;211&gt; 807

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 189

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&lt;210&gt; 190

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 190

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 <213> Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

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acaatcatta	gctcaggcaa	ttggaagcca	aattgaagat	gccaggcggt	gcagcggagc	660
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gcaagtttca	agattgggaa	gtta				744

&lt;210&gt; 194

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 194

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&lt;210&gt; 195

&lt;211&gt; 771

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 195

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&lt;210&gt; 196

&lt;211&gt; 561

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 196

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&lt;210&gt; 197

&lt;211&gt; 691

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 197

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&lt;210&gt; 198

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 198

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&lt;210&gt; 199

&lt;211&gt; 811

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 199

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&lt;210&gt; 200

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 200

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&lt;210&gt; 201

&lt;211&gt; 717

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 201

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&lt;210&gt; 202

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 202

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tcctagangc	tgctagacac	agcgggcagc	actggganaa	gagaagggaa	gctgcggggag	540
gcgccaaccc	gtcatgccag	gggacagtgt	ganagtcacg	ggncgggcta	ngccaatggg	600
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&lt;210&gt; 203

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 203

cagccatgga	cgccatcaag	aagaagatgc	agatgctgaa	gctggacaag	gagaacgcca	60
tcgaccgcgc	cgagcaggcc	gaagccgaca	agaagcaagc	tgaggaccgc	tgcaagcagc	120
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agtattctga	atccgtgaag	gaggcccagg	agaaactgga	gcaggccgag	aagaaggcca	240
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cggaggagan	ggctgaggtg	gccgagagcc	gagccagaca	gctggaggag	gaacttcgaa	600
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acctta						786

&lt;210&gt; 204

&lt;211&gt; 738

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 204

ggctagtaac	atcagtttta	ttgggttggg	gtggcaacca	tagcctggct	gggggtgggg	60
ctggccctca	caggttgttg	agttccagca	gggtctggtc	caaggctctg	tgaatctcga	120
cgttctcttc	cttggcactg	gccaaggtct	cttctaggtc	atcgatgggt	ttctccaact	180
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acagtttgat	ctcctcttca	tatttatctt	ctttgggtgga	atactcctcc	tctgaggcca	300
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tctcgggcac	ctcagccctc	tcctccgagc	gctccagctc	tccttcagag	atcaccagct	420
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aaggaaggca	anatctgctt	caacaacaat	tggccttctt	cncggccngc	tccaattttc	720
ncngggggcc	tccttcaa					738

&lt;210&gt; 205

&lt;211&gt; 818

&lt;212&gt; DNA



&lt;213&gt; Homo Sapiens

&lt;400&gt; 205

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gttctcctcc	ttggcactgg	ccaagggtctc	ttctaggtca	tcgatgggtt	tctccaactt	180
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cagtttgatc	tcctcttcat	atttatcttc	tttgggtggaa	tactcctcct	ctgaggccat	300
cagggacttg	agggcctggg	ccatgggttcg	aagttcctcc	tccagctgtc	tggctcggct	360
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nctngcncca	attttctccn	ggggcctncc	tttcangggg	tnaagaanaa	atttcaaatt	780
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&lt;210&gt; 206

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 206

cagccatgga	cgccatcaag	aagaagatgc	agatgctgaa	gctggacaag	gagaacgcca	60
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agtattctga	atccgtgaag	gaggcccagg	agaaactgga	gcaggccgag	aagaaggcca	240
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cggctgatga	gagcgagaga	ggaatgaagg	tcatcgaaaa	ccgggccatg	aaggatgagg	420
agaagatgga	actgcaggag	atgcagctga	aggaggccaa	gcacatcgct	gaggattcag	480
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tggaaactcaa	caacctgtga	gggccagccc	cacccccagc	caggctatgg	ttgccacccc	900
aaccaataa	aactgatgtt	actagcc				927

&lt;210&gt; 207

&lt;211&gt; 910

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 207

ggaagatggc	ggcggccggt	ccacagcggg	cgtggaccgt	ggagcagctg	cgcagtgagc	60
agctgccccaa	gaaggacatt	atcaagtctc	tgcaggaaca	cggttcagat	tcgtttcttg	120
cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
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gagataaaaac	caactttccc	aaaaagggag	atgttgttca	ctgctggtat	acaggaacac	420
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aaggaaaaag	tcaactggga	aaaattcaag	gnggttaana	aaaanttggt	ttacctgggg	840
ccaagcctt	ttngaaaaa	aaaanccct	tatgaaancc	ccngggccca	aaaanacttt	900
tccnaaaacc						910

&lt;210&gt; 208

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 208

gacagtggat	caattttttat	tgagccactt	aagtttacia	catgaggtaa	aaggaaaaag	60
ttctccttga	ccagtatttt	acacagctgt	aggaaagtat	tttagaccag	ggattcataa	120
gggattttatc	tctcaaaaag	tgggaccaag	taaacaaatt	ttattaactc	cttgaatttt	180
ccagttgact	cttcctttac	aatagtaaca	agttctaact	agttgtgtaa	atctcttcaa	240
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tatccactaa	ttccacttca	aaagtgagtt	ttgcatttgg	tgggaattttg	gcacagggt	360
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tacntggccn	cagacacttt	tactt				745

&lt;210&gt; 209

&lt;211&gt; 965

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 209

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cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
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gtaaagtgtc	tgagcaagta	aaaaatgtga	agcttaatat	agataaaacc	aaagaaacca	300
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aaact						965

&lt;210&gt; 210

&lt;211&gt; 867

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 210

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aagttctcct	tgaccagtat	tttacacagc	tgtaggaaag	tatttttagac	cagggattca		120
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nccttangtt	ttaaaaaaaa	tgggttataa	gggctggtaa	ccnaagggtg	ggcccttggt		840
aaccngttct	tggggcaaaa	tttttaa					867

&lt;210&gt; 211

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 211

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tgatccactg	tc					972

&lt;210&gt; 212

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 212

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&lt;210&gt; 213

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 213

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agaattttcn	ccntttggga	tnaattaaca	agttgc			756

&lt;210&gt; 214

&lt;211&gt; 728

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 214

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&lt;210&gt; 215

&lt;211&gt; 710

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 215

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acaagctagg	aagtcttcaa	accttgagtt	gaattccana	aggggttatt	tggcttttga	300
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ctttcttggc	atgatgagcc	tgtanaactg	ctacagcttc	atccaccttg	gagcgganag	420
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&lt;210&gt; 216

&lt;211&gt; 824

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 216

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&lt;211&gt; 749

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 217

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&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 221

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&lt;210&gt; 222

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 222

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&lt;210&gt; 223

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 223

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&lt;210&gt; 224

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 224

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&lt;210&gt; 225

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 225

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&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 229

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&lt;210&gt; 230

&lt;211&gt; 842

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 230

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&lt;210&gt; 231

&lt;211&gt; 781

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 231

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&lt;210&gt; 232

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 232

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gatcggagnc	atgacacatg	ttaacctaa	nacangactg	gagggtttac	ncangaagat	720
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&lt;210&gt; 233

&lt;211&gt; 879

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 233

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&lt;210&gt; 234

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 234

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&lt;210&gt; 235

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 235

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&lt;210&gt; 236

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 236

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711

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<211> 658

<212> DNA

<213> Homo Sapiens

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<210> 238

<211> 678

<212> DNA

<213> Homo Sapiens

<400> 238

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<211> 1402

<212> DNA

<213> Homo Sapiens

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&lt;210&gt; 240

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 240

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&lt;210&gt; 241

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 241

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 <213> Homo Sapiens

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 <213> Homo Sapiens

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&lt;210&gt; 245

&lt;211&gt; 592

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 245

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&lt;211&gt; 821

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 246

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&lt;211&gt; 639

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 247

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&lt;210&gt; 248

&lt;211&gt; 846

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 248

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&lt;210&gt; 249

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 249

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&lt;210&gt; 250

&lt;211&gt; 899

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 250

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&lt;210&gt; 251

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 251

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&lt;210&gt; 252

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 252

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753

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&lt;210&gt; 256

&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 256

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&lt;210&gt; 257

&lt;211&gt; 885

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 257

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&lt;210&gt; 258

&lt;211&gt; 798

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 258

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&lt;210&gt; 259

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 259

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&lt;211&gt; 772

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 260

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&lt;211&gt; 661

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 264

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&lt;211&gt; 659

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 265

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&lt;210&gt; 266

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 266

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&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 267

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&lt;210&gt; 268

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 268

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 269

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&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 270

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&lt;211&gt; 814

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 271

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&lt;211&gt; 862

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;213&gt; Homo Sapiens

&lt;400&gt; 273

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&lt;210&gt; 274

&lt;211&gt; 863

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 274

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 278

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&lt;210&gt; 279

&lt;211&gt; 702

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 279

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